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(54) Title: ANTIGENIC POLYPEPTIDES

(57) Abstract: The invention relates to a method for the identification of antigenic polypeptides, typically opsonic antigens, expressed by pathogenic microbes; vaccines comprising said antigens; and therapeutic antibodies directed to said antigenic polypeptides.

INTERNATIONAL SEARCH REPORT

Intern al Application No
PCT/GB 02/03606

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C07K7/04 C07K14/195 C07K16/12 A61K39/02 A61P31/04

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C07K A61K A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, BIOSIS, EMBASE, EMBL, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL [Online] 16 March 1999 (1999-03-16), BARASH ET AL: "Staphylococcus aureus polynucleotides and sequences" XP002250642 retrieved from AAW89789 accession no. EBI Database accession no. AAW89789 * Refers to EP-A-786519, published 30.07.97 (3271 pages); identical with Locus 1, Sequence 3 [4-363 : 2-361]; and SEQ 544 (EP), complete reversed DNA overlap [1400-5088 : 3689-1/Locus 1] * ----- -/--	1-7, 9-16, 18-26

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
8 August 2003	17 11 2003

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Korsner, S-E.

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
X	DATABASE EMBL [Online] 1 June 2001 (2001-06-01), KURODA ET AL: "Whole genome sequencing of meticillin-resistant Staphylococcus aureus" XP002250643 retrieved from Q99WI0 accession no. EBI Database accession no. Q99WI0 * 98% overlap in the region 21-251 [Locus 1, Sequence 4] : 1-231; misfits at 49, 83,141,144 and 229 (of Q99WI0) * -----	
P,X	WO 01 98499 A (UNIVERSITY OF SHEFFIELD / BIOSYNEXUS) 27 December 2001 (2001-12-27)	1-7, 9-16, 18-26
P,Y	* See the whole document - antigenic polypeptides from Staphylococcus aureus; SEQ.ID. 32 = identical with Locus 1, Sequence 1; page 5 -> SEREX * -----	27
Y	SAHIN ET AL: "Serological identification of human tumor antigens" CURRENT OPINION IN IMMUNOLOGY, vol. 9, no. 5, October 1997 (1997-10), pages 709-716, XP004313590 ISSN: 0952-7915 * The original SEREX method / see page 5 of the Application * -----	27
A	US 6 159 469 A (CHOI ET AL) 12 December 2000 (2000-12-12) * See Abstract - antigenic polypeptides from Streptococcus pneumoniae * -----	1-26
A	US 6 086 896 A (SPARLING ET AL) 11 July 2000 (2000-07-11) * See Abstract - antigenic polypeptide from Neisseria meningitidis * -----	1-26
A	US 5 543 323 A (RIDLEY ET AL) 6 August 1996 (1996-08-06) * See Abstract - antigenic polypeptides from Plasmodium * -----	1-26
A	WOOD ET AL: "Identification of antigenic sites on staphylococcal enterotoxin B and toxoid" FEMS IMMUNOLOGY AND MEDICINAL MICROBIOLOGY, vol. 17, 1997, pages 1-10, XP002250576 * See pages 8-9 (3.3 and 4) * -----	1-26

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INTERNATIONAL SEARCH REPORT

Inten al Application No
PCT/GB 02/03606

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
L	DATABASE EMBL [Online] 20 February 2003 (2003-02-20), MASIGNANI ET AL: "Staphylococcus aureus proteins and nucleic acids" XP002250644 retrieved from AX618827 accession no. EBI Database accession no. AX618827 * Refers to WO02094868, published 28.11.02 (international filing date 27.03.02, priority date 27.03.01) without sequences (electronically filed only) - see Locus 1, Sequence 1 = 100% identity * -----	1-26
L	DATABASE EMBL [Online] 20 February 2003 (2003-02-20), MASIGNANI: "Staphylococcus aureus proteins and nucleic acids" XP002250645 retrieved from AX618829 accession no. EBI Database accession no. AX618829 * As above; identical with Locus 1, Sequence 2 (except the first amino acid) * -----	1-26
L	DATABASE EMBL [Online] 20 February 2003 (2003-02-20), MASIGNANI: "Staphylococcus aureus proteins and nucleic acids" XP002250646 retrieved from AX618833 accession no. EBI Database accession no. AX618833 * As above; identical with Locus 1, Sequence 3 (except the first amino acid) * -----	1-26
L	DATABASE EMBL [Online] 20 February 2003 (2003-02-20), MASIGNANI: "Staphylococcus aureus proteins and nucleic acids" XP002250647 retrieved from AX618835 accession no. EBI Database accession no. AX618835 * As above; identical with Locus 1, Sequence 4 (except the first amino acid; erroneous omission of 241-251 ?) * -----	1-26

INTERNATIONAL SEARCH REPORT

International application No.
PCT/GB 02/03606

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

see FURTHER INFORMATION sheet PCT/ISA/210

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-26 (all partially) and 27 (entirely)

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

Although Claims 12-17 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the polypeptides/compositions.

Note also that "or part thereof" (Claim 1) has no clear meaning - it would even cover dipeptides in an extreme interpretation.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination before the EPO (see EPO Guideline C-VI, 8.5), should the problems which led to the Article 17(2) declaration be overcome.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-26 (all partially) and 27 (entirely)

Invention 1:

Claim 27 (the method used) and a first group of antigenic polypeptides (the 4 peptides of Locus 1, encoded by the first DNA sequence in Table 7), including their uses etc. as of dependent Claims 2-26, as applicable.

Inventions 2-134:

As invention 1 but limited to each subsequent group of peptides as encoded by the 2nd, 3rd,..., 122th DNA sequence

in Table 7, and the 123th,..., 134th DNA sequence in Table 9, as applicable.

Note:

As a consequence of the lack of information in the Description about sequence relations (e.g. common subsequences ?) etc, the actual number of inventions may deviate from the above.
This is, however, not of significance at present.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Inte Application No
PCT/GB 02/03606

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 0198499 A	27-12-2001	AU 7424801 A	02-01-2002
		BR 0111823 A	10-06-2003
		CA 2412504 A1	27-12-2001
		CN 1437653 T	20-08-2003
		EP 1292681 A1	19-03-2003
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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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WO 03/011899 A2

(54) Title: ANTIGENIC POLYPEPTIDES

(57) Abstract: The invention relates to a method for the identification of antigenic polypeptides, typically opsonic antigens, expressed by pathogenic microbes; vaccines comprising said antigens; and therapeutic antibodies directed to said antigenic polypeptides.

Antigenic Polypeptides

The invention relates to a method for the identification of antigenic polypeptides, typically opsonic antigens, expressed by pathogenic microbes; vaccines comprising said antigens; and therapeutic antibodies directed to said antigenic polypeptides.

Microbial organisms cause a number of fatal or debilitating diseases which affect many millions of people around the world. Currently methods to control microbial organisms include the use of antimicrobial agents (antibiotics) and disinfectants. These have proved to be problematic since exposure to these agents places a significant selection pressure resulting in the creation of resistant microbes which can avoid the effects of the antimicrobial agent(s). For example, recently it has been discovered that microbial organisms have become resistant to triclosan, an agent added to many disinfectants used in households and industrial environments.

An arguably greater problem is the evolution of antibiotic resistant strains of a number of significant pathogenic microbes.

For example, and not by way of limitation, it is estimated that there are up to 50 million people world-wide infected with drug resistant tuberculosis (TB) (Figures from the World Health Organisation, 1998). In the past the use of antibiotics to treat TB relied on the administration of single drugs (eg ethionamide) which promoted a relatively high frequency of resistance. For this reason, combinations of drugs are now used to treat tuberculosis. However the fatality rate in cases caused by strains that are resistant to at least one drug used to treat tuberculosis still approaches 50% even when treatment is given. *Mycobacterium tuberculosis*, the causative agent of TB, is a slow growing bacteria and takes a long time to kill. Therefore, for a drug combination to be effective a person with TB must take the drug combination daily for at least six months. Accordingly, patients frequently have to take two or more pills daily and this requires a regimented dosage over a relatively long period of treatment. Many patients take the medications only intermittently and therefore do

not finish the full course of therapy [illegible] infection. Moreover, TB is strongly associat[illegible] establishment of TB is strongly correlated with imm[illegible]

[illegible]berculosis

Vaccination against TB has been available for many years. Therefore the guerin (BCG) vaccination has been widely used throughout the world because it is a safe and inexpensive means to vaccinate large numbers of p[illegible] potentially could contract TB. BCG is derived from live, attenuated strains *Mycobacterium bovis*. However the impact of vaccination on the infectious forms of TB is minimal and BCG has therefore contributed little to the overall control of the disease.

A further example of a pathogenic organism which has developed resistance to antibiotics is *Staphylococcus aureus*. *S.aureus* is a bacterium whose normal habitat is the epithelial lining of the nose in about 20-40% of normal healthy people and is also commonly found on people's skin usually without causing harm. However, in certain circumstances, particularly when skin is damaged, this germ can cause infection. This is a particular problem in hospitals where patients may have surgical procedures and/or be taking immunosuppressive drugs. These patients are much more vulnerable to infection with *S.aureus* because of the treatment they have received. Resistant strains of *S.aureus* have arisen in recent years. Methicillin resistant strains are prevalent and many of these resistant strains are also resistant to several other antibiotics. Currently there is no effective vaccination procedure for *S. aureus*. In the US, *S.aureus* infections are the cause of 13% of the two million hospitalised infections each year. This represents 260,000 people with an infection of *S.aureus*, of which 60-80,000 die.

S. aureus is therefore a major human pathogen capable of causing a wide range of life threatening diseases including septicaemia, endocarditis, arthritis and toxic shock. This ability is determined by the versatility of the organism and its arsenal of components involved in virulence. Pathogenicity is multifactorial and no one

component has shown to be responsible for a particular infection, see Projan, S.J. & Novick, R.P. (1997) in The Staphylococci in Human Disease (Crossley, K.B. & Archer, G.L., eds.) pp.55-81.

At the onset of infection, and as it progresses, the needs and environment of the organism changes and this is mirrored by a corresponding alteration in the virulence determinants which *S. aureus* produces. At the beginning of infection it is important for the pathogen to adhere to host tissues and so a large repertoire of cell surface associated attachment proteins are made. These include collagen-, fibrinogen- and fibronectin-binding proteins. The pathogen also has the ability to evade host defences by the production of factors that reduce phagocytosis or interfere with the ability of the cells to be recognised by circulating antibodies.

Often a focus of infection develops as an abscess and the number of organisms increases. *S. aureus* has the ability to monitor its own cell density by the production of a quorum sensing peptide. Accumulation of the peptide, associated with physiological changes brought about by the beginning of starvation of the cells, elicits a switch in virulence determinant production from adhesins to components involved in invasion and tissue penetration. These include a wide range of hemolysins, proteases and other degradative enzymes.

During the process of any infection the virulence determinants made by *S. aureus* are produced in response to environmental and physiological stimuli. These stimuli will be dependent on the niche within the body and will change as the infection progresses. Little is known of the conditions *in vivo* and it is likely that some components are produced solely in this environment. These are therefore potential vaccine components, which could not be discovered by previous techniques.

One of the most important developments in recent medical history is the development of vaccines which provide prophylactic protection from a wide variety of pathogenic organisms. Many vaccines are produced by inactivated or attenuated pathogens which are injected into an individual. The immunised individual responds by producing both a humoral (antibody) and cellular (cytolytic T cells, CTL's) response. For example, hepatitis vaccines are made by heat inactivating the virus and treating it with a cross linking agent such as formaldehyde. An example of an attenuated pathogen useful as a vaccine is represented by polio vaccines which are produced by attenuating a live pathogen.

However the use of attenuated organisms in vaccines for certain diseases is problematic due to the lack of knowledge regarding the pathology of the condition and the nature of the attenuation. For certain viral agents this is a particular problem since viruses, in particular retroviruses, have an error prone replication cycle which results viable mutations in the genes which comprise the virus. This can result in alterations to antigenic determinants which have previously been used as vaccines. An alternative to the use of inactivated or attenuated pathogens is the identification of pathogen epitopes to which the immune system is particularly sensitive. In this regard many pathogenic toxins produced by pathogenic organisms during an infection are particularly useful in the development of vaccines which protect the individual from a particular pathogenic organism.

The development of so-called subunit vaccines (vaccines in which the immunogen is a fragment or subunit of a protein or complex expressed by a particular pathogenic organism) has been the focus of considerable medical research. The need to identify candidate molecules useful in the development of subunit vaccines is apparent not least because conventional chemotherapeutic approaches to the control of pathogenic organisms has more recently been stymied by the development of antibiotic resistance. A number of methods have been developed to identify potential antigenic polypeptides which can be used as a vaccine. One such method is disclosed herein.

It has been known for many years that tumour cells produce a number of tumour cell specific antigens, some of which are presented at the tumour cell surface. The immune system recognises these antigens as foreign thereby resulting in the production of antibodies to self antigens, so called autoantibodies or autologous antisera.

One such technique is Serological identification of antigens by recombinant Expression Cloning, abbreviated to SEREX.

Typically, the technique involves the extraction of RNA from tumour tissue followed by the selective enrichment of mRNA from the isolated total RNA. The mRNA is reverse transcribed into cDNA using viral reverse transcriptase. The cDNA thus synthesised is subcloned into an expression vector and transformed into an appropriate bacterial strain. The transformed bacteria are plated onto a suitable nutrient agar and under appropriate growth conditions the subcloned cDNA is expressed from the expression vector in the bacterial cell. The cells are lysed naturally by the use of phage based expression vectors, for example λ phage or phagemid based vectors, which through their lytic cycle cause cell lysis. The released polypeptides are transferred to a suitable membrane support (i.e. nitrocellulose, nylon) and exposed to autologous antisera from the patient from which the tumour tissue was originally isolated. The immunoscreening methodology allows the identification of genes that are over expressed or inappropriately expressed in a selected tumour tissue from a patient.

We have exploited this techinque to identify antigenic polypeptides expressed by pathogenic organisms during an infection. Autologous antisera produced during the infection is used to screen an expression library created from genomic DNA to identify and clone antigens.

In its broadest aspect the invention relates to the identification of antigenic polypeptides expressed during an infection by a pathogenic microbe and their use in vaccination.

According to a first aspect of the invention there is provided a method to identify opsonic antigens expressed by pathogenic organisms comprising:

(i) providing a nucleic acid library encoding genes or partial gene sequences of a pathogenic organism;

(ii) transforming/transfecting said library into a host cell;

(iii) providing conditions conducive to the expression of said transformed/transfected genes or partial gene sequences;

(iv) contacting the antigens expressed by the genes/partial gene sequences with autologous antisera derived from an animal infected with, or has been infected with, said pathogenic organism;

(v) purifying the nucleic acid encoding the antigens or partial antigenic polypeptides binding to said autologous antisera; and

(vi) testing the opsonic activity of a polypeptide encoded by said DNA molecule.

In a preferred method of the invention said library comprises genomic DNA of a pathogenic organism.

Ideally said pathogenic organism is bacterial.

More preferably still said bacterial organism is selected from the following: *Staphylococcus aureus; Staphylococcus epidermidis; Enterococcus faecalis; Mycobacterium tuberculsis; Streptococcus group B; Streptoccocus pneumoniae; Helicobacter pylori; Neisseria gonorrhea; Streptococcus group A; Borrelia*

burgdorferi; Coccidiodes immitis; Histoplasma sapsulatum; Neisseria meningitidis type B; Shigella flexneri; Escherichia coli; Haemophilus influenzae.

Preferably still said pathogenic organism is of the genus *Staphylococcus spp.* Ideally organism is *Staphylococcus aureus* or *Staphylococcus epidermidis.*

In a further preferred embodiment of the invention said nucleic acid library is a lambda library, ideally a lambda expression library.

According to a second aspect of the invention there is provided a nucleic acid molecule comprising a DNA sequence selected from:

(i) the DNA sequence as represented by the DNA sequences herein disclosed in Table 7 or Table 9;

(ii) DNA sequences which hybridise to the sequences identified in (i) above which encode a polypeptide expressed by a pathogenic organism and

(iii) DNA sequences which are degenerate as a result of the genetic code to the DNA sequences defined in (i) and (ii).

In a yet still further preferred embodiment of the invention said nucleic acid molecule is genomic DNA.

In a preferred embodiment of the invention there is provided an isolated nucleic acid molecule which anneals under stringent hybridisation conditions to the sequences herein disclosed.

Stringent hybridisation/washing conditions are well known in the art. For example, nucleic acid hybrids that are stable after washing in 0.1xSSC, 0.1% SDS at 60°C. It

is well known in the art that optimal hybridisation conditions can be calculated if the sequences of the nucleic acid is known. For example, hybridisation conditions can be determined by the GC content of the nucleic acid subject to hybridisation. Please see Sambrook *et al* (1989) Molecular Cloning; A Laboratory Approach. A common formula for calculating the stringency conditions required to achieve hybridisation between nucleic acid molecules of a specified homology is:

$T_m = 81.5^0\ C + 16.6\ Log\ [Na^+] + 0.41[\ \%\ G + C] - 0.63\ (\%formamide)$.

According to a third aspect of the invention there is provided at least one polypeptide identified by the method according to the invention.

In a preferred embodiment of the invention, said polypeptide is associated with infective pathogenicity of an organism according to any previous aspect or embodiment of the invention.

More preferably still said polypeptide is at least one, or part part thereof, of the amino acid sequences represented in Tables 8 or Table 10.

In an alternative preferred embodiment of the invention said polypeptide carries a non-protein antigen, for example a polysaccharide antigen.

According to a fourth aspect of the invention there is provided a nucleic acid molecule characterised in that said nucleic acid molecule is part of a vector adapted to facilitate recombinant expression of the polypeptide encoded by said nucleic acid molecule.

In a preferred embodiment of the invention said vector is an expression vector adapted for prokaryotic gene expression. Alternatively said expression vector is adapted for eukaryotic gene expression.

Typically said adaptation includes, by example and not by way of limitation, the provision of transcription control sequences (promoter sequences) which mediate cell specific expression. These promoter sequences may be cell specific, inducible or constitutive.

Promoter is an art recognised term and, for the sake of clarity, includes the following features which are provided by example only, and not by way of limitation. Enhancer elements are *cis* acting nucleic acid sequences often found 5' to the transcription initiation site of a gene (enhancers can also be found 3' to a gene sequence or even located in intronic sequences and is therefore position independent). Enhancers function to increase the rate of transcription of the gene to which the enhancer is linked. Enhancer activity is responsive to *trans* acting transcription factors (polypeptides) which have been shown to bind specifically to enhancer elements. The binding/activity of transcription factors (please see Eukaryotic Transcription Factors, by David S Latchman, Academic Press Ltd, San Diego) is responsive to a number of environmental cues which include, by example and not by way of limitation, intermediary metabolites (eg glucose, lipids), environmental effectors (eg light, heat,).

Promoter elements also include so called TATA box and RNA polymerase initiation selection (RIS) sequences which function to select a site of transcription initiation. These sequences also bind polypeptides which function, *inter alia*, to facilitate transcription initiation selection by RNA polymerase.

Adaptations also include the provision of selectable markers and autonomous replication sequences which both facilitate the maintenance of said vector in either the eukaryotic cell or prokaryotic host. Vectors which are maintained autonomously are referred to as episomal vectors.

Adaptations which facilitate the expression of vector encoded genes include the provision of transcription termination/polyadenylation sequences. This also includes

the provision of internal ribosome entry sites (IRES) which function to maximise expression of vector encoded genes arranged in bicistronic or multi-cistronic expression cassettes.

These adaptations are well known in the art. There is a significant amount of published literature with respect to expression vector construction and recombinant DNA techniques in general. Please see, Sambrook et al (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbour Laboratory, Cold Spring Harbour, NY and references therein; Marston, F (1987) DNA Cloning Techniques: A Practical Approach Vol III IRL Press, Oxford UK; DNA Cloning: F M Ausubel et al, Current Protocols in Molecular Biology, John Wiley & Sons, Inc.(1994).

According to yet a further aspect of the invention there is provided a method for the production of the polypeptides according to any previous aspect or embodiment of the invention comprising:

(i) providing a cell transformed/transfected with a vector according to the invention;

(ii) growing said cell in conditions conducive to the manufacture of said polypeptides; and

(iii) purifying said polypeptide from said cell, or its growth environment.

In a preferred method of the invention said vector encodes, and thus said recombinant polypeptide is provided with, a secretion signal to facilitate purification of said polypeptide.

According to a fifth aspect of the invention there is provided a cell or cell-line transformed or transfected with the vector according to the invention.

In a preferred embodiment of the invention said cell is a prokaryotic cell. Alternatively said cell is a eukaryotic cell selected from: fungal, insect, amphibian; mammalian; plant.

According to a yet further aspect of the invention there is provided a vaccine comprising at least one antigen or antigenic polypeptide according to the invention.

Ideally said vaccine further comprises a carrier and/or adjuvant.

The terms adjuvant and carrier are construed in the following manner. Some polypeptide or peptide antigens contain B-cell epitopes but no T cell epitopes. Immune responses can be greatly enhanced by the inclusion of a T cell epitope in the polypeptide/peptide or by the conjugation of the polypeptide/peptide to an immunogenic carrier protein such as key hole limpet haemocyanin or tetanus toxoid which contain multiple T cell epitopes. The conjugate is taken up by antigen presenting cells, processed and presented by human leukocyte antigens (HLA's) class II molecules. This allows T cell help to be given by T cell's specific for carrier derived epitopes to the B cell which is specific for the original antigenic polypeptide/peptide. This can lead to increase in antibody production, secretion and isotype switching.

An adjuvant is a substance or procedure which augments specific immune responses to antigens by modulating the activity of immune cells. Examples of adjuvants include, by example only, agonsitic antibodies to co-stimulatory molecules, Freunds adjuvant, muramyl dipeptides, liposomes. An adjuvant is therefore an immunomodulator. A carrier is an immunogenic molecule which, when bound to a second molecule augments immune responses to the latter.

In yet a further aspect of the invention there is provided a method to immunise an animal against a pathogenic microbe comprising administering to said animal at least one polypeptide, or part thereof, according to the invention or the vaccine according to the invention.

In a preferred method of the invention said animal is human.

Preferably the vaccine, or antigenic polypeptide, can be delivered by direct injection either intravenously, intramuscularly, subcutaneously. Further still, the vaccine or antigenic polypeptide, may be taken orally.

Preferably the vaccine is against the bacterial species *Staphylococcus aureus.*

The vaccine may also be against the bacterial species *Staphylococcus epidermidis.*

It will also be apparent that vaccines or antigenic polypeptides are effective at preventing or alleviating conditions in animals other than humans, for example and not by way of limitation, family pets, livestock, horses.

According to a further aspect of the invention there is provided an antibody, or at least an effective binding part thereof, which binds at least one antigen or antigenic polypeptide according to the invention.

In a preferred embodiment of the invention said antibody is a polyclonal or monoclonal antibody wherein said antibody is specific to said polypeptide.

Alternatively, said antibody is a chimeric antibody produced by recombinant methods to contain the variable region of said antibody with an invariant or constant region of a human antibody.

In a further alternative embodiment of the invention, said antibody is humanised by recombinant methods to combine the complimentarity determining regions of said antibody with both the constant (C) regions and the framework regions from the variable (V) regions of a human antibody.

Preferably said antibody is provided with a marker including a conventional label or tag, for example a radioactive and/or fluorescent and/or epitope label or tag.

Preferably said humanised monoclonal antibody to said polypeptide is produced as a fusion polypeptide in an expression vector suitably adapted for transfection or transformation of prokaryotic or eukaryotic cells.

Antibodies, also known as immunoglobulins, are protein molecules which have specificity for foreign molecules (antigens). Immunoglobulins (Ig) are a class of structurally related proteins consisting of two pairs of polypeptide chains, one pair of light (L) (low molecular weight) chain (κ or λ), and one pair of heavy (H) chains (γ, α, μ, δ and ε), all four linked together by disulphide bonds. Both H and L chains have regions that contribute to the binding of antigen and that are highly variable from one Ig molecule to another. In addition, H and L chains contain regions that are non-variable or constant.

The L chains consist of two domains. The carboxy-terminal domain is essentially identical among L chains of a given type and is referred to as the "constant" (C) region. The amino terminal domain varies from L chain to L chain and contributes to the binding site of the antibody. Because of its variability, it is referred to as the "variable" (V) region.

The H chains of Ig molecules are of several classes, α, μ, σ, α, and γ (of which there are several sub-classes). An assembled Ig molecule consisting of one or more units of two identical H and L chains, derives its name from the H chain that it possesses. Thus, there are five Ig isotypes: IgA, IgM, IgD, IgE and IgG (with four sub-classes based on the differences in the H chains, i.e., IgG1, IgG2, IgG3 and IgG4). Further detail regarding antibody structure and their various functions can be found in, Using Antibodies: A laboratory manual, Cold Spring Harbour Laboratory Press.

Chimeric antibodies are recombinant antibodies in which all of the V-regions of a mouse or rat antibody are combined with human antibody C-regions. Humanised antibodies are recombinant hybrid antibodies which fuse the complimentarity determining regions from a rodent antibody V-region with the framework regions from the human antibody V-regions. The C-regions from the human antibody are also used. The complimentarity determining regions (CDRs) are the regions within the N-terminal domain of both the heavy and light chain of the antibody to where the

majority of the variation of the V-region is restricted. These regions form loops at the surface of the antibody molecule. These loops provide the binding surface between the antibody and antigen.

Antibodies from non-human animals provoke an immune response to the foreign antibody and its removal from the circulation. Both chimeric and humanised antibodies have reduced antigenicity when injected to a human subject because there is a reduced amount of rodent (i.e. foreign) antibody within the recombinant hybrid antibody, while the human antibody regions do not illicit an immune response. This results in a weaker immune response and a decrease in the clearance of the antibody. This is clearly desirable when using therapeutic antibodies in the treatment of human diseases. Humanised antibodies are designed to have less "foreign" antibody regions and are therefore thought to be less immunogenic than chimeric antibodies.

In a further preferred embodiment of the invention said antibodies are opsonic antibodies.

Phagocytosis is mediated by macrophages and polymorphic leukocytes and involves the ingestion and digestion of micro-organisms, damaged or dead cells, cell debris, insoluble particles and activated clotting factors. Opsonins are agents which facilitate the phagocytosis of the above foreign bodies. Opsonic antibodies are therefore antibodies which provide the same function. Examples of opsonins are the Fc portion of an antibody or compliment C3.

In another aspect of the invention there is provided a vector which is adapted for the expression of the humanised or chimeric antibodies according to the invention.

In a yet further aspect of the invention, there is provided a cell or cell line which has been transformed or transfected with the vector encoding the humanised or chimeric antibody according to the invention.

In a yet further aspect of the invention there is provided a method for the production of the humanised or chimeric antibody according to the invention comprising :

(i) providing a cell transformed or transfected with a vector which comprises a nucleic acid molecule encoding the humanised or chimeric antibody according to the invention;

(ii) growing said cell in conditions conducive to the manufacture of said antibody; and

(iii) purifying said antibody from said cell, or its growth environment.

In a yet further aspect of the invention there is provided a hybridoma cell line which produces a monoclonal antibody as hereinbefore described.

In a further aspect of the invention there is provided a method of producing monoclonal antibodies according to the invention using hybridoma cell lines according to the invention.

In a further aspect of the invention there is provided a method for preparing a hybridoma cell-line producing monoclonal antibodies according to the invention comprising the steps of:

i) immunising an immunocompetent mammal with an immunogen comprising at least one polypeptide having the amino acid sequence as represented in Table 8 or 10, or fragments thereof;

ii) fusing lymphocytes of the immunised immunocompetent mammal with myeloma cells to form hybridoma cells;

iii) screening monoclonal antibodies produced by the hybridoma cells of step (ii) for binding activity to the amino acid sequences of (i);

iv) culturing the hybridoma cells to proliferate and/or to secrete said monoclonal antibody; and

v) recovering the monoclonal antibody from the culture supernatant.

Preferably, the said immunocompetent mammal is a mouse. Alternatively, said immunocompetent mammal is a rat.

The production of monoclonal antibodies using hybridoma cells is well-known in the art. The methods used to produce monoclonal antibodies are disclosed by Kohler and Milstein in Nature 256, 495-497 (1975) and also by Donillard and Hoffman, "Basic Facts about Hybridomas" in Compendium of Immunology V.II ed. by Schwartz, 1981, which are incorporated by reference.

In a further aspect of the invention there is provided the use of the antibodies for manufacture of a medicament for the treatment of *Staphylococcus aureus*-associated septicaemia, food-poisoning or skin disorders.

In another aspect of the invention there is provided the use of the antibodies according to the invention for the manufacture of a medicament for the treatment of *Staphylococcus epidermidis*-associated septicaemia, peritonitis or endocarditis.

It will be apparent that the polypeptides identified by the method according to the invention will facilitate the production of therapeutic antibodies to a range of diseases resulting from pathogenic infection, for example, septicaemia; tuberculosis; bacteria-associated food poisoning; blood infections; peritonitis; endocarditis; sepsis; meningitis; pneumonia; stomach ulcers; gonorrhoea; strep throat; streptococcal-associated toxic shock; necrotizing fasciitis; impetigo; histoplasmosis; Lyme disease; gastro-enteritis; dysentery; shigellosis.

As has already been stated earlier, microbial organisms cause a wide variety of diseases. Listed below, and not by way of limitation, are a number of micro-organisms and some of the diseases they cause.

Micro-organism	**Disease(s) caused**
Staphylococcus aureus	Sepsis, food poisoning, septicaemia,
Staphylococcus epidermidis	Peritonitis, septicaemia, endocarditis,

	other hospital-associated diseases
Enterococcus faecalis	Endocarditis, cystitis, wound infections
Mycobacterium tuberculosis	Tuberculosis
Streptococcus group B	Sepsis, meningitis, pneumonia, bladder infections
Streptococcus pneumoniae	Pneumonia, meningitis
Helicobacter pylori	Stomach ulcers
Neisseria gonorrhoea	Gonorrhoea
Streptococcus group A	Strep throat, necrotizing fasciitis, impetigo, Strep. Toxic shock syndrome
Borrelia burgdoferi	Lyme disease
Coccidiodes immitis	Pneumonia
Histoplasma sapsulatum	Histoplasmosis, pneumonia
Neisseria meningitidis type B	Meningitis
Shigella flexneri	Gastro-enteritis, shigellosis, dysentry
Escherichia coli	Food-poisoning, gastro-enteritis
Haemophilus influenzae	Meningitis, pneumonia, arthritis, cellulitis

An embodiment of the invention will now be described by example only and with reference to the following materials, methods and tables:

Table 1 illustrates the immunization and bleed schedule for production of monoclonal antibodies reactive with peptide Hex A;

Table 2 illustrates an immunoassay of sera from mice immunized with peptide Hex A;

Table 3 illustrates an immunoassay of supernatants from anti-Hex A hybridoma supernatants;

Table 4 illustrates the immunization and bleed schedule for production of monoclonal antibodies reactive with peptide 29kDa peptide;

Table 5 illustrates an immunoassay of day 98 sera from mice immunized with peptide 29kDa;

Table 6 illustrates an immunoassay of supernatants from anti-29kDa hybridomas supernatants from T75 Culture Flasks;

Table 7 represents the DNA sequences of *S.aureaus* partial gene sequences identified by the screening method;

Table 8 represents the protein sequences encoded by the DNA sequences illustrated in Table 7;

Table 9 represents the DNA sequences of *S.epidermidis* partial gene sequences identified by the screening method; and

Table 10 represents the protein sequences of the DNA sequences illustrated in Table 9.

Materials and Methods

Screening Genomic Libraries of *S. aureus* and *S.epidermidis*

A λZAP Express library of genomic DNA of *S. aureus* 8325/4 and *S.epidermidis* was used. It contains fragments of 2-10kb from a partial *Sau*3A digest of total genomic DNA. This was cloned into the *Bam*H1 site of the vector. The library contains >10x coverage of the genome. The library was probed by plaque lift using an initial screen of approximately 20,000 plaque forming units on a 9cm diameter Petri dish. The plating cells used, their treatment, the plating procedure and buffers were exactly as described in the manufacturers handbook (Stratagene). Plating cells, *Escherichia coli* XL1-Blue MRF', were infected with phage and plated in 3 ml top LB agar containing 10 mM $MgSO_4$ onto LB plates containing 10 mM $MgSO_4$. The plates were then incubated at 42°C for 4 hr. An 8.5cm diameter nitrocellulose filter disc (previously soaked in 10 mM IPTG and air-dried) was placed on each plate and its location marked. The plates were then incubated for a further 3.5 hr at 37°C. The

filters were removed and washed in TBST buffer before blocking overnight at 4°C in TBST containing 6% w/v dried skimmed milk and 3% v/v pig serum (Sigma). The serum was used to block any Protein A clones on the filter. The filters are then treated with patient serum (1/5000 dilution) in blocking solution for 90 min at room temperature. Antisera have been obtained from patients convalescing from major *S. aureus* infections. The filters are then washed for 3x10 min in TBST. Secondary antibody used was goat anti-human whole IgG alkaline phosphatase linked (Sigma) at 1/30,000 dilution in blocking solution at room temperature for 30 min. The filters were then washed as above and developed using a standard colorimetric procedure.

Cross-reactive plaques were located on the agar plates and cored into 0.2ml phage buffer with 0.02 ml chloroform. The titre of each core stock was determined and the phage plated at approximately 200 plaques per plate. A plaque lift and screen was performed as above to give single, pure cross-reactive clones.

The pure clones were then spotted (1µl) onto plates to give a confluent plaque of 0.5cm diameter. 30 individual clones can be spotted on each plate. A plaque lift is performed and the filter probed with an appropriate sera. In this way clones can be tested for their cross-reactivity with other patient sera, non-infected donor sera and anti-Protein A sera.

Individual clones were then excised to give a phagemid in *E. coli* XLOLR using the manufacturers protocol (Stratagene). A plasmid miniprep of each was carried out and the size of the genomic insert determined by restriction mapping. The identity of the cloned insert was determined by DNA sequencing using primers against vector sequence, which allows sequencing across the insert. By comparison of the derived sequence against the public domain databases the nature of the cloned gene(s) can be determined.

Hybridisation Solutions/Conditions

Typically, hybridisation conditions uses 4 – 6 x SSPE (20x SSPE contains 175.3g NaCl, 88.2g NaH_2PO_4 H_2O and 7.4g EDTA dissolved to 1 litre and the pH adjusted to 7.4); 5-10x Denhardts solution (50x Denhardts solution contains 5g Ficoll (type 400, Pharmacia), 5g polyvinylpyrrolidone abd 5g bovine serum albumen; 100μg-1.0mg/ml sonicated salmon/herring DNA; 0.1-1.0% sodium dodecyl sulphate; optionally 40-60% deionised formamide. Hybridisation temperature will vary depending on the GC content of the nucleic acid target sequence but will typically be between 42^0- 65^0 .

Mouse Model for Testing Candidate Vaccine Polypeptides

Mice are injected intravenously with 5 x 10^7 S. aureus and mortality, bacteremia and abscess formation is monitored over the ensuing 7 days. At this dose 100% of the mice are bacteremic for greater than 4 days , 100% have detectable abscess formation in liver and kidney and greater than 80% of mice die within four days. At lower doses of injected organisms, bacteremia is detectable in the absence of death.

Immunization Program

Single proteins are injected at a dose of 10-100ug per mouse in RIBI adjuvant, boosted 14 and 28 days later and bled 14 and 28 days thereafter for evaluation of antibodies in their sera using ELISA. When groups of proteins are injected the final amount of each protein will be 10ug per mouse and the above immunization scheme will be followed.

Evaluation of Protective Efficacy of Single or Groups of Proteins

We will employ the mouse infection model described above to evaluate the protective efficacy of the proteins that are being tested. To this end groups of 5 mice will be immunized with single proteins or pools of 5 proteins as described above. We will monitor antibody titers to the injected proteins and when high titers are reached we will inoculate mice with *S aureus* at high and low dose. Control mice that have

not been immunized or that were immunized with adjuvant only will also be inoculated with *S aureus*. We will measure levels of bacteremia,abscess formation and survival in all groups. All parameters of infection will be suppressed in mice that have high circulating levels of protective antibodies. If we find a pool of proteins that induces protection we will compare the protection induced by the individual components to that induced by the pool of proteins to see if protection was induced by a single protein or by the combined action of antibodies to multiple proteins. Using this approach we will identify protein epitopes that are protective.

In addition to using the *in vivo* model of mouse infection we will also obtain the sera from mice that are injected as above and monitor their sera for opsonophagocytic activity using a complement dependent system in the presence of human polymorphonuclear lymphocytes. This assay is well known in the art. This assay has been used an *in vitro* surrogate for measuring protective efficacy of antibody. Spleens from mice that have opsonophagocytic antibodies will then be used as fusion partners in an attempt to make monoclonal antibodies that are reactive with *S. aureus* .

Using this multipronged approaches we will have a high level of confidence that we can identify protective epitopes that can be used either in a vaccine construct or that can be used to generate monoclonal antibodies.

EXAMPLE 1

Immunoassay for detection of antibodies reactive with peptide Hex A

The binding of mouse sera or MAbs to Hex A was measured by immunoassay on wells coated with Hex A. One hundred microliters of a 250 – 500 ng/ml solution of Hex A in PBS was distributed into replicate Nunc Maxisorp Stripwells and incubated overnight at room temperature. The unbound material was removed from the wells by washing four times with PBS-T. Unbound antigen was removed from the plate by washing four times with PBS-T. Antibody, diluted in PBS-T, was then added to the wells and incubated at room temperature for 30-60 minutes. After addition of the antibody, the wells were incubated at room temperature for 30-60 minutes in a draft-

free environment. The wells were again washed four times with PBS-T and ninety-five microliters of detection antibody was then added to each well. The detection antibody was either peroxidase-labeled goat anti-mouse IgG (gamma-specific), diluted 1:10000 in PBS-T, or peroxidase-labeled rabbit anti-mouse IgG_1, diluted 1:6000 in PBS-T.

Following another 30-60 minute incubation at room temperature, the wells were washed four times with PBS-T and each well received 100 µl of TMB substrate solution (BioFx #TMBW-0100-01). Plates were incubated in the dark at room temperature for 15 minutes and the binding reactions were stopped by the addition of 100 µl of TMB stop solution (BioFx #STPR-0100-01). The absorbance of each well was measured at 450 nm using a Molecular Devices Vmax plate reader.

Isotype was determined using a mouse immunoglobulin isotype kit obtained from Zymed Laboratories (Cat. No. 90-6550).

Immunization of Mice for Production of Monoclonal Antibodies Reactive with Peptide Hex A.

Five female BALB/c mice, approximately 8 weeks of age, were immunized with Hex A according to the schedule described in Table I. All immunizations were administered subcutaneously in 50% RIBI adjuvant. Sera from the mice were tested by immunoassay, and based on the results of the assay described in Table 2, mouse 2021 was selected for hybridoma production. Mouse 2021 received a booster immunization of 32.5 ug of Hex A in PBS, administered intraperitoneally, three days prior to the production of hybridomas.

TABLE 1

Immunization and Bleed Schedule for Production of Monoclonal Antibodies Reactive with Peptide Hex A

Experimental Day		Boost (ug/mouse)	Adjuvant		Bleed
0		10 ug	RIBI		Yes
34		8.3	RIBI		Yes
48		None			Yes
60		25 ug	RIBI		Yes
74		None			Yes
98		25 ug	RIBI		Yes
124		None			Yes

TABLE 2

Immunoassay of Sera from Mice Immunized with Peptide Hex A

Serum Dilution	2021	2022	2023	2024	2025
1000	3.553	3.569	3.226	3.336	3.439
3000	2.803	2.538	2.357	2.575	2.403
9000	1.663	1.336	1.314	1.522	1.357
27000	0.793	0.618	0.622	0.716	0.598
Buffer	0.095	0.078	0.145	0.066	0.089

Preparation of Hybridomas Reactive with Hex A Peptide

Hybridomas were prepared by the general methods of Shulman, Wilde and Kohler and Bartal and Hirshaut (34, 48). Mouse 2021 was selected for hybridoma production based on the results of an immunoassay and received a booster immunization of 32.5 ug of antigen three days prior to sacrifice. Spleenocytes from

mouse 2028 were isolated and mixed with mouse myeloma cells SP2/0 (ATCC Catalog number CRL 1581) at a ratio of 10 spleenocytes:1 myeloma. The cells were pelleted by centrifugation (400 X g, 10 minutes at room temperature) and washed in serum free medium. The supernatant was removed to near-dryness and fusion of the cell mixture was accomplished in a sterile 50 ml centrifuge conical by the addition of 1 ml of warm (37°C) polyethylene glycol (PEG; mw 1400; Boehringer Mannheim) over a period of 60-90 seconds. The PEG was diluted by slow addition of serum-free medium in successive volumes of 1, 2, 4, 8, 16 and 19 mls. The hybridoma cell suspension was gently resuspended into the medium and the cells pelleted by centrifugation (500 X g, 10 minutes at room temperature). The supernatant was removed and the cells resuspended in medium RPMI 1640, supplemented with 15% heat-inactivated fetal bovine serum, 0.05 mM hypoxanthine and 16 μM thymidine (HT medium). One hundred μl of the hybridoma cells were planted into 952 wells of 96-well tissue culture plates. Eight wells (column 1 of plate A) received approximately 2.5 X 10^4 SP/20 cells in 100 μl. The SP/20 cells served as a control for killing by the selection medium added 24 hours later:

Twenty four hours after preparation of the hybridomas, 100 μl of RPMI 1640, supplemented with 15% heat-inactivated fetal bovine serums, 0.1 mM hypoxanthine, 0.8 μM aminopterin and 32 μM thymidine (HAT medium) was added to each well. Ninety-six hours after the preparation of the hybridomas, the SP/20 cells in plate A, column 1 appeared to be dead, indicating that the HAT selection medium had successfully killed the unfused SP/20 cells.

Ten days after the preparation of the hybridomas, supernatants from all wells were tested by ELISA for the presence of antibodies reactive with peptide Hex A. Based on the results of this preliminary assay, cells from three wells were transferred to a 24-well culture dish and expanded. Supernatants from these cultures were retested by ELISA for the presence of antibodies that bind to peptide Hex A.

Using IgG-1-specific detection, the absorbance values obtained with the supernatants from hybridoma culture 02-101FE1, 02-101ED8 and 02-100JC10 were 2.150, 2.230 and 2.574, respectively, compared to an absorbance of 0.044 with buffer alone (Table 3). Absorbances were lower, but still positive, with gamma-specific detection (Table 3). Each of the cultures was expanded, cryopreserved and cloned by limiting dilution. Two-three clones of each culture were expanded and cryopreserved for future evaluation.

TABLE 3

Immunoassay of Supernatants from Anti-Hex A Hybridoma Supernatants

		Detection With	Detection With
Culture ID	**Dilution**	**Anti-Mouse IgG-1**	**Anti-Mouse Gamma**
02-101FE1	2	2.150	0.941
02-101JC10	2	2.574	1.403
02-101ED8	2	2.238	1.174
Buffer		0.044	0.073

EXAMPLE 2

Immunoassay for detection of antibodies reactive with peptide 29kDa

The binding of mouse sera or MAbs to 29kDa was measured by immunoassay on wells coated with 29kDa. One hundred microliters of a 500 - 1000 ng/ml solution of 29kDa in PBS was distributed into replicate Nunc Maxisorp Stripwells and incubated overnight at room temperature. The unbound material was removed from the wells by washing four times with PBS-T. Unbound antigen was removed from the plate by washing four times with PBS-T. Antibody, diluted in PBS-T, was then added to the wells and incubated at room temperature for 30-60 minutes. After addition of the antibody, the wells were incubated at room temperature for 30-60 minutes in a draft-

free environment. The wells were again washed four times with PBS-T and ninety-five microliters of detection antibody was then added to each well. The detection antibody was either peroxidase-labeled goat anti-mouse IgG (gamma-specific), diluted 1:10000 in PBS-T, or peroxidase-labeled rabbit anti-mouse IgG_1, diluted 1:6000 in PBS-T.

Following another 30-60 minute incubation at room temperature, the wells were washed four times with PBS-T and each well received 100 µl of TMB substrate solution (BioFx #TMBW-0100-01). Plates were incubated in the dark at room temperature for 15 minutes and the binding reactions were stopped by the addition of 100 µl of TMB stop solution (BioFx #STPR-0100-01). The absorbance of each well was measured at 450 nm using a Molecular Devices Vmax plate reader.

Isotype was determined using a mouse immunoglobulin isotype kit obtained from Zymed Laboratories (Cat. No. 90-6550).

Immunoassay for detection of antibodies reactive with peptide 29kDa

The binding of mouse sera or MAbs to 29kDa was measured by immunoassay on wells coated with 29kDa. One hundred microliters of a 500 - 1000 ng/ml solution of 29kDa in PBS was distributed into replicate Nunc Maxisorp Stripwells and incubated overnight at room temperature. The unbound material was removed from the wells by washing four times with PBS-T. Unbound antigen was removed from the plate by washing four times with PBS-T. Antibody, diluted in PBS-T, was then added to the wells and incubated at room temperature for 30-60 minutes. After addition of the antibody, the wells were incubated at room temperature for 30-60 minutes in a draft-free environment. The wells were again washed four times with PBS-T and ninety-five microliters of detection antibody was then added to each well. The detection antibody was either peroxidase-labeled goat anti-mouse IgG (gamma-specific), diluted 1:10000 in PBS-T, or peroxidase-labeled rabbit anti-mouse IgG_1, diluted 1:6000 in PBS-T.

Following another 30-60 minute incubation at room temperature, the wells were washed four times with PBS-T and each well received 100 µl of TMB substrate solution (BioFx #TMBW-0100-01). Plates were incubated in the dark at room temperature for 15 minutes and the binding reactions were stopped by the addition of 100 µl of TMB stop solution (BioFx #STPR-0100-01). The absorbance of each well was measured at 450 nm using a Molecular Devices Vmax plate reader.

Isotype was determined using a mouse immunoglobulin isotype kit obtained from Zymed Laboratories (Cat. No. 90-6550).

Immunization of Mice for Production of Monoclonal Antibodies Reactive with Peptide 29kDa

Five female BALB/c mice, approximately 8 weeks of age, were immunized with 29kDa according to the schedule described in Table 1. All immunizations were administered subcutaneously in 50% RIBI adjuvant. Sera from the mice were tested by immunoassay, and based on the results of the assay described in Table 2, mouse 2028 was selected for hybridoma production. Mouse 2028 received a booster immunization of 50 ug of 29kDa in PBS, administered intraperitoneally, three days prior to the production of hybridomas.

TABLE 4

Immunization and Bleed Schedule for Production of Monoclonal Antibodies Reactive with Peptide 29kDa

Experimental Day		Boost (ug/mouse)	Adjuvant		Bleed
0		10 ug	RIBI		Yes
34		10 ug	RIBI		Yes
48		None			Yes
60		20 ug	RIBI		Yes
74		None			Yes
98		20 ug	RIBI		Yes

TABLE 5

Immunoassay of Day 98 Sera from Mice

Immunized with Peptide 29kDa

Mouse ID		Sera at 1:1000		Sera at 1:10000	
2026		0.260		0.078	
2027		1.415		0.306	
2028		2.184		0.383	
2029		0.838		0.107	
2030		1.073		0.154	
Buffer		0.061			

Preparation of Hybridomas Reactive with 29kDa Peptide

Hybridomas were prepared by the general methods of Shulman, Wilde and Kohler and Bartal and Hirshaut (34, 48). Mouse 2028 was selected for hybridoma production based on the results of an immunoassay and received a booster immunization of 50 ug of antigen three days prior to sacrifice. Spleenocytes from mouse 2028 were isolated and mixed with mouse myeloma cells P3X63Ag8.653 (ATCC Catalog number CRL 1580) at a ratio of 10 spleenocytes:1 myeloma. The cells were pelleted by centrifugation (400 X g, 10 minutes at room temperature) and washed in serum free medium. The supernatant was removed to near-dryness and fusion of the cell mixture was accomplished in a sterile 50 ml centrifuge conical by the addition of 1 ml of warm (37°C) polyethylene glycol (PEG; mw 1400; Boehringer Mannheim) over a period of 60-90 seconds. The PEG was diluted by slow addition of serum-free medium in successive volumes of 1, 2, 4, 8, 16 and 19 mls. The hybridoma cell suspension was gently resuspended into the medium and the cells pelleted by centrifugation (500 X g, 10 minutes at room temperature). The supernatant was removed and the cells resuspended in medium RPMI 1640, supplemented with 15% heat-inactivated fetal bovine serum, 0.05 mM hypoxanthine and 16 μM thymidine (HT medium). One hundred μl of the hybridoma cells were

planted into 952 wells of 96-well tissue culture plates. Eight wells (column 1 of plate A) received approximately 2.5 X 10^4 P3X63Ag8.653 cells in 100 µl. The P3X63Ag8.653 cells served as a control for killing by the selection medium added 24 hours later.

Twenty four hours after preparation of the hybridomas, 100 µl of RPMI 1640, supplemented with 15% heat-inactivated fetal bovine serums, 0.1 mM hypoxanthine, 0.8 µM aminopterin and 32 µM thymidine (HAT medium) was added to each well. Ninety-six hours after the preparation of the hybridomas, the P3X63Ag8.653 cells in plate A, column 1 appeared to be dead, indicating that the HAT selection medium had successfully killed the unfused P3X63Ag8.653 cells.

Ten days after the preparation of the hybridomas, supernatants from all wells were tested by ELISA for the presence of antibodies reactive with peptide 29kDa.. Based on the results of this preliminary assay, cells from 3 wells were transferred to a 24-well culture dish and expanded. Several days later, supernatants from these cultures were retested by ELISA for the presence of antibodies that bind to peptide 29kDa.

The absorbance values obtained with the supernatants from hybridoma cultures 02-100EC7, 02-100HH10 and 02-100FG5 are presented in Table 3. Based on these results, cultures 02-100EC7 and HH10 were expanded, cryopreserved and cloned by limiting dilution. Two-three clones of each culture were expanded and cryopreserved for future evaluation.

TABLE 6

Immunoassay of Supernatants from Anti-29kDa Hybridomas

Supernatants from T75 Culture Flasks

Culture ID	Culture Dilution	Detection With Anti-Mouse IgG-1	Detection With Anti-Mouse Gamma
02-100HH10	2	1.021	0.312
02-100EC7	2	0.687	0.230
02-100FG5	2	0.048	0.048
Buffer Alone		0.044	0.050

TABLE 7
LOCUS 1 (E8/B1/I16)
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TGACATCTGCCATGCGATTTTCTTGTAATTTTTTGTGCAATTCAAACGTGTACTTTCCAC
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AGCTCTTTCAAGGAAATCTCTTCCTTAGTAATCATGTATTCTGAAACATCGCGTGAAATC
ATACCTTGATTATCTTTTTTAGTAATGCTTAATTCTACTTTGTGATTAACTTTTTTACTA
TTAGTCTTCGTGATGCCACCGACAGAATATTTTTTCAATTGATATTTATTGTCTTCTAAA
ACGATAAATACATCGATATTATCGTAAGGTCCATCTTTATATTTTTTCTCATCTTTTCCA

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LOCUS 2 (B10/I15)

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LOCUS 3
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LOCUS 4 (E103)
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LOCUS 5 (L4)
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LOCUS 6 (D1)
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LOCUS 7 (D3)

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LOCUS 8 (D4)
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LOCUS 9A (D22)
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GCAAGCGTGGTTAAACAGAAACAACAAAGTAATAATGAACAGACTGAGAATCGAGAATCT
CAAGTACAAAATTCTCAAAATTCACAAAATGGTCAATCATTATCTGCTACTCATGAAAAT
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TTTTTTGATGCAAATTATCATGATTATCGCTTTATTGACCGTGAAAATGCAGATTCTGGC
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C

LOCUS 9C (J13)
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LOCUS 9D (M11)
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LOCUS 9E (M13)
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ACGAAAGATCAAGTTACTGAAGCGATGAATCAAGTGAATTCTGCTAAAAATAACTTAGAT
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LOCUS 10 (D9)

GATCGTCGGCTAAAACTTGATGTGTTACATCTAAACCAAACACATTTATAGTAATCCCAC
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LOCUS 11 (D10)

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LOCUS 12 ()

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LOCUS 13 (D18)

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GGATTTAAAAAAAGCCATTGCTGAACTATTAGCAATACAAATGTTATAAACCCCATAAAT
CCATTAAATGCCAGAAAATGTTTGACATATGTTTTAGCTGACATGTGTTCTAAATCTGTG
CCGATAATTTTAAAACACATATTTTCAAATCTAGTAAATATTAAATCTACTCTTGACGAT
TGCACCAATGCTACGCGATATAGATATCCACTAAAAACATACGTAATCATAACCATCATT
GTTAGAAACAAAATTATTTCCATGATAACCCTCACTTAATATATTTCTAAAATTTTTCAC
TACGAATTAAGGCATAAAATAAATACAAAACTAATGCAATAACTACCAGTAATAAAACGA
TGAGCATTGCCATAACCTCCTTACAACACAACAACATCGTAACAACTTGTTTATGAGAGA
AATATTAATTTTCAAACTTAGTTATTAAGAAATCATTAAGATGTGTATGCAGAAATAAAT
TTTATAGCATTTAATTGTGAAGAATATTATGATATTGCTATCGAGGTGAAGGTTATGTCA
AACACTGAATCGCTAAACATAGGAAAAAAGCGTGGATC

LOCUS 14 (D21)

GATCACTGCATCTCCATCATTAACACCGTCATTTTGATTCTCAACGATGAATGGTACTAC
GAATTCGTCAGTTAAGCCCTCATTATAGCTTGCTTCTACACCTTCTTTGGCAGTTGCATA
AGTTGGGGCATCAAAATTACGAATAGCATTGTAAGCTTTTTCTTCACGTTCCCAACGTTT
GTCACGATCCATTGCATAATAACGACCAGACACAGATGCAAATTGACCAATGCCTAATTC
ATTGAATTTAGCTTCAGTCTCTTCGATGTATTTCAAAGCGGATTTTTGATCTACGTCACG
GCCATCTAAAAATGCGTGTACGTAAACTTTTTCAACACCTTGTTTTTTTAGCAAGTTCTAA
CAAAGCAAATAAATGTTTGTAATGACTGTGTACACCACCGTCAGACAATAAACCAAAGAT
GTGTAACGCTGAATCATGTGAATTCACGTGTGCAATTGCATTATTTAAAACATCATTTTC
AAAGAAATCACCGTCTTCAATTGATTTATTGATTCGAGTTAAACTTTGATAAACGATACG
TCCTGCACCGATATTCATATGACCAACTTCTGAGTTACCCATTTGTCCTTCAGGTAGTCC
AACATCTAAGCCACTCGCTTCGATTTGAGTCGTTGGATATTTGTTGTAATAACGATCAAA
ATTAGGCTTGTTTGCTAATTTTACCGCATTACCATGTTCGCTTTCGCGGTTCGCAAAACC
ATCTAAAATAATTAACGCAGTTGGTTTCTTAGCCATGATTATTTTGCACCTTCTAACAAT
TGTACGAAATCTTCAACTTTAAGTGATGCGCCACCTACTAATGCCCCATCAATATCAGTT
TGTGCCATGTATTCTTTAATGTTGTTAGGTTTAACACTACCACCATATTGAATACGAGTT
GCTTCTGATACTTCTTTGCTTGATAAGTCAGCAATAGTTTGACGTACAAATGCACACATT
TCATTTGCATCTTCAGATGTTGATGATTTACCAGTTCCGATTGCCCAGATTGGTTCATAA

GCAATTACAACTGATTTAAGTTGATCTTCAGATAAACCTGCAACAGCTTTCTTAACTTGC
TCACCTACAACATCGTTAGCTTTACCACTTTCACGCTCTTCGTCTGTTTCACCAACACAT
ATAATTGGAGTCATTCCATGTTTGAAAATAGCGTGCGCTTTTTTGTTAATTTCTTCATCT
GTTTCGTGGAATAATTCACGACGTTCAGAATGACCGATAACAACGTATTTAACGCCTAAA
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TCTAATTGAATTGCTGGTGCACAAATTACTGATTCTACTTCTTTTGAATCTGGTAGTGTT
GGTAATGTATTGACGAAGTCTTTTGCTTCTTGTACTGTTTTGTTCATTTTCCAGTTACCA
GCTATAATTGGTGTTCTCATTAAAGACACTCCTTGTTTTGTAAATATTTTTGAAAAGTGA
TGAAACACGATGTCATCTTGTGACTGTTTTCCCGTAACAATGTTAAACAAACATGCCACA
TCACTTTAAACTATCACTTTATTATTTATTATTGATTGCTTTGATACCAGGCAATTCTTT
ACCTTCTAGGTACTCTAATGACGCGCCGCCACCAGTTGAAATATGAGTGAAGTCATTTTC
AAAACCTAAAGAGATTGCTGCTGCAGCTGAATCACCGCCACCGATAATCGTAATTGCATC
TTTAAGGTTTGCAATTGCTTTACATACACCAATTGTACCTTGTGCAAAGTTACTGAACTC
GAATACACCCATAGGTCCATTCCATACAACAGTGTGCGCACCTTCTAATTCATCTGCAAA
TAATTTTACAGTGTTTGGTCCAATATCCATACCTTCTTGGTCTGCTGGAATTGAATCAGA
TGGTACTACAGTGATTTTGGCATCATTAGAAAATTCTTTAGCAACTTTAGTGTCTACTGG
TAATACAATTTTATCACCATGTTTTTCTAATAAATCTTTTGCGAAGTCGATTTTATCTTC
TTCTAATAATGAAATACCAATTTCTTTACCTTGCGCTTTTAAGAAAGTATAAGCCATACC
TCCGCCGATGATAATTTTATCAGCTATGTTAACTAAGTTTTTGATGACATTAATTTTGTC
AGATACTTTTGCTCCACCTAAAATAGCAACAACTGGTTTATGTGGATCGTTAACTACGCC
GCCAATAAACTTAATTTCTTTATCCATTAAGAATCCAGCTGCAGTTTCTAAATGTGTAGA
AATACCAACATTAGATGCATGCTCACGATGCGCAGTACCAAAAGCATCATTTACAAACAC
ATCACCTAAAGATGCCCAGTATTTACCTAATTCTGGATC

LOCUS 15 (I1)

GATCCTGAAACGTAATTAATTGAAACTGTAGAACCTTCAGTCACCTTGTTGTCTTTTCTA
ATCACTACTACTGGTAAATTTAAAATATTAGCAACCGCATTTGCCAATGAAATACCTTTT
GTCGCAATGGTAACAACAGCATCTAATTTTTCTTCCATGTAAATACTGGCAATTAACTTA
CCAACTTTGTTTAGTAGCGATGGATTACCTACCAAATCTGATAAAAATAAATATCCGCCA
GGTAACAAACGTTCTTTCTCTTCTAATAGAGTAATGACCTCATTAACAACTTCAGTCGCC
TCTTCTTTACTCATCATTGGTTTATACGTAACACCACCACTTGCGCCAGCAGTAGTAATT
ACTGTACCTAACTTTTCTTTTTGGAATGTATTTTTTATAATTTGGACATCTTCACTTATT
GAAGACTTCGCCTGTTTAAATTTTTTCACAAAAAAAGTTAATGGAATCAATTTATTCGGA
TGGTTCATCAAATATTGCGTCATAAAAACAATTCTCTCGCTTCGTTTATATCTCATCTTT
TCAACCCTTCTATCCTAATAGTCTAACTAAGTACACTTCATTACAACAACCGTTAACTGC
ATTATAAATATTTTTTGCTTGGCTTTCTTTTCGTGCTAGCCCATACACAGTAGGTCCGCT
TCCACTCATTAACGCACCATCTGCACCACTTTTCAACATATTATTTTTTAATTTATCGAT
TTGTGGGTGTTTTGAAACAGAAATTGGCTCTAATCGATTAGACAAACTTTGACATAATTG
TTGATAATCTCGATTTTCTAAGGCCTCATAACACATTTTCGTATGTACGTCGTAACGCTT
ATCTAAATTAATCAACTTAAATATATCTGGTGATGATATGCCTAAGTTTGGTTTAGCAAG
AATCACCCAAGCTGAAGGTGGTTTATTTAAAAACTCGATTTTCTCTCCTCTTCCAGTACA
TAGTGCAGTTTTATTATAAATACAAAACGGAATATCTGTCCCGATTTTACTGCCTAGTAG
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TGCTGCATCAGCCGAACCTCCAGCTAAGCCAGCAGAAACAGGTATTTCTTTATCGATAGA
AATTGTTACACCTTGCTTTAGTTGATATTGCTCAATAAATAGTTGCGCTGCACGATATGC
GAGATTTTTATGATTAGAAGGCACATAATTATGTTCAATCTCAACAACTATCTTTCGATC
TTTTCTTTTATGAAAAGTTAAACGATC

LOCUS 17 (I3)

GATCGACAACACTCTAAATATATAGAAAATAGGTATTAATTTAACTATAAATCTAAATAA

TAATGCAAAGATGATTAAAATAACGATAGCTAAAGCAATACCAATAATAAAATCTTTGGT
CGCTAGCTCACCTATCATCCCCATATAGAAAATGATAACCTCGACACCTTCACGCAACAC
AGATATTAAACCAATCGTCGCTAACAATACCAAATTACCATTACTAATCGCATTAGCATA
CATATTTTTAATCATGTCATTCCAACGTTTTGCATTTGAACGTTTGTGCATCCAAACACC
AACGATAAACATTAATATGACCGCAACGATACCTAATCCCGCTTCCATACTTTCACGAAG
AATGCCACTATTCCCTAAAGTTTCTACAAACGTAATTGCTAAGATAATACTCAGTACAAG
TCCGGCAATTGCACCACCAATCACACTTGCAGTCCCTTTCTTATCTTTTACATTACGCGT
CATGGTAGTCAATGTCATTACAATTAACAACACTTCTAGCCCTTCACGTAAAAAGATAAT
CATCACATCGACGAAGCTATAACTATGGCCAACAACCTCTTTAATTTGGTTATTTAAATC
TACTAAACCATCTTTCACATGTGCTTTATTATGTTCGTCTAATACACTTTGATAATATGG
TATTTTATCTTCAATTTTCGTATACAAAGCACCGTCTTTAGTTTGAATTTGACCTTCAAC
ATACGGCCAAGTTTCTATAAAATGTGTAAGCGCAGCATCAGCATCCGACAATTGATTGTC
GTCGATAGCTTTAATCGCCTTCTCTAACGCATCATTTAATTGTGATACATGGTATTGATC
ATTTGCAGACGTATTACTTTTTTTATCGACATGATCAATATTTGATTTAAAAGTTGTCCA
AGCATGTGACACTTTTGCCGTATCTAATGGTGACTTATGAATTGCAATTCTAAGTTGTAA
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CAAATAATGTTTCACCAAGGTATCCTCCCTTACTAACACCTGGTAATACTAAAAATGAAG
CAGAACCTCTATGTGTAATATATTCATTTAATTTATCATTACTACCTAAATTATTTTGTA
TATCGATAAATTGTTTTGTCGCTTTTTGAAAAGCAATAAAAAGTAAGCCTGTTTCGAAGT
TACCTGTGCGGTCATCCGTACCATCCACATAATTAAAGGCTCTACGTAAAATTGACGTAT
TTGCTTCTTTCGCTAGCCTCGTATGGGCATCTTTATCAATAATATACTCGCCATGACTAT
CTTTCGCTTTTAAGTCAATTTCATCAAACTCTTTCCCACCTGTTAACGGTGCACCACTAT
GTCGTTTCCGACCAAATGTAGCCTCTTGTTCTTCCAGCGCAGTACGATC

LOCUS 18 (IS)

GATCGTTTAAATGTTCAATATATTCCGCTGCACTTTGCGCTGCAATACTACCATCGCCAG
TAGCAGTGACAATTTGGCGTAAACCTTTGTCGCGAACATCTCCTGCTGCAAAAATACCTG
GTACTGATGTTGTCATATCATCTTTTGTTACAATATAACCAACATCATTTGTAATACCTA
AGTCTTTAAATGGCGCTGTTAATGGTTTCATACCAATATAGATGAATACACCATCAGCCT
CGTGTGTTTCTTCTGAACCATCTTTTGTAGACGTTAATGTCACAGAACCCACTTTGCCGT
CTTTTTCATTAATTGATTTCAAAGTATGACTCCAAATAAAGTCGATTTTATCATTTTTGA
ATGCTCTATCTTGTAAAATACGCTGTGCACGTAACTCATCACGACGGTGAACGATTGTTA
CTTTGTCAGCAAATTTAGTTAAGAATGTTCCCTCTTCTACTGCTGAATCACCACCACCGA
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CGCGTCCACCAAGTTCTTGTTCACCCGGAACACCAATTTTCTTGTATTCTGCACCTGTAG
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GCGCATTATATAATAAATCTAACTTTTCATAAATCTATATGCTCAAGAGAAATTCAATCA
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CTAATTTATTGAGCGTTAAACCTTGAACTAAATACGTTAAATACAATTTCTCATAATTAT
TTAGATTTTCCAAAACCTGCCAAATACTTTCCGTCATCACAATTTCTTTACCATTTAATT
GATC
LOCUS 19 (I8)
GATCGTTGATTTGATTAGTGATGGTTGAACAAATTAAAAATAAACTACTTACTGCAAATA
CTACGCCCATAACGATAAACGTAGTAGCTGGTGTAGTATAACTTGTAATGGCAGCGCCAC
TAAGACTGCCAATAATTTGACCAACAACTAACATACTGTTCGTCGTTCCAACAAATGTGC
CTTTAAGTTGTTGATGACACGCATTCACGACAACAAACATGACACTTTGAATCAATGCAC
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CGGACTGTAAAAATCCAATCACACTACGGTCATCTATCGCTGTATGATTCACTGATGAAG
CAAGTGGTGATAATGCAGTTAGCATGCCATACATAGCAAAGTTTGCTAAAACGCCAACGA
TAATAAATCGACATGTTTGTTGTGTGCATAATAGACATTGAAATGAACGGCGAATACCTT
TATTAATATTTGGTGTTTGTGATTTTGGCATATGTGTCGTTTCAATCAATTTTAATGCAC
CGAAAATACAGACAATAAAAGTAATAACGGCAATACTCATCAGTAACGCACTAAAACCTA
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CACTTGATGCATCAACAACACCACCAAATAGTCCCTGCAATAACCTCACAAGTACAAACT
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CTGATAGATTTTGTAGTGATGCCATATAAATTGGCAATAATGGCACAAGTACTGTCAGTC
CAGCAATCGCTATAAACTGACTGAGCCATAAAATGCGAAAGTTACTGCGCCATATAGACT
GATTAATCATATGTCACCATTGGATTTGGTACGGTAGTTAAACCTGAAGGCATACTACCT
CCACCACTATCACGTTGATATAGCAATGGTAATAAAATTTGTTTGAATGGCCACGTCTGT
TTATCAAATAAAATGTGTCTGACAGCTAGCTGATCAGTTGTAACCCAGGAAATAGTTGCC
ACTTCATTTTTTAAAATTTGTTTTAACAACGACATAAGTTCATGCTCACTTACACCAAAT
AAATCTTGAATTGCATCAATAATGGCATATAGATTTACCGATACAGCTAATGTTTGAAAA
TAAGCAAAGAATGTTTCCAAATCCTCATTAATTAGCGTATTAGGTGTATCTTCTCTGACG
ACATACTTCGGCAATGAAAGCTGATGTGCTGTTAGCCATGGTTTATAAATTCTGACAGTA
TCATGATCACGTAACACGCATTTTTGTACACGTCCATCTTCAAATGACAACAATATATTT
TGACCATGCAACTCTGGTAATGCGCCGTATTGCATAAATGATAGTGTTACCTTTAAAAAG
ACTTGCGCGATATCTTCAAATAACGTCATGACATCATTTTTAGAAATATTATCTTTTCCA
CAAATCATTTGATATAAAGTGCGATCATTTGCCGCGAGTGCTGCCATTGACACTAGCTGT
TGCGTATCATTTTTGGCTAGCACTTCGGGATACTTTCTTAGCTGAACAGTTAGATGACCT
AATTGATCTTTGAAAATATCATTATCTTGACCCATATATGACCACCAAGCTGTTTCATCA
CAAACCATGACATACTTAGCTAGTGCTTCATCTTTTTCTATAAGCTGACGTAATAATTGT
TCTGCTTGTTCTCCGTTTTTCATGTAACGCGTAGGCGTTAGCCTTAATGCGCCTAATGAC
TGCATTGCAAATGGTACTTTGACATGGTTATACGGTGCGCCAATATCAATTAATGAACGC
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TGTGTCTTTTTAACTGCTGCAACCATTAAAGGAAATGATTGATTTAATTCAGCTTGATAC
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TCTTTTAAACTTGCAAACTGCTCTGACATCACAAAAGGATGTGACGCTAAATCTAATTCT
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TCCCATTCATGACTTAGATCACAATTCATATTAGCAATTGTTTGCCAAAATTCAGCTGCC

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AACATATTTAAAGCACTAAAATAAACAGGTATCTTTATTTGTTGTGTTTCACGTTCGTAT
ATCAAAAGCGTTTGTCCGTTTTCTTTAGTAATCTCACTATTCGATACAATTCCGGCTATA
TCTTCAAATAATAATGCATCAACTAAATCTCTTAATATTATCGCTTGTGCTGTATTGACT
GCTGTATGATTCTGCAATGTTCAGACACCTCGCATTCTTAATATAGGTTCAATGTTGTCC
CAATATTTTGTTGTTGTGCCTGTTGATAAATAAAATAAGCACTTGAAATATCTTCGATAG
CCATACCCATCGGATTAAGTAATATGATC

LOCUS 20 (J7/M10)

GATCGCTTACAAAACATAACAAGCTTTAAAGATATTGCCAAAATTCTTTATTCAACGAGA
GCAGGCGTTGCTTATATGGCTACAGGTGGTATGGCTGGCGCTTTACGTGCCACATTAGAT
TATGTCACTGAGCGTAAGCAATTCGGCAAACCAATTAGTAAATATCAGTTAATACAAGAA
AAGCTAGCAATGATGCAAGGTAATTTAGCTCAAGCAATGGCAACATGTGCTCAATTAGCT
AATATGCAAGCACATGGTGAATATGACGAGGTTGCAACTTCAACGGCGAAGATGATGAAT
GCCTTACGTTTGCGTGAGACAGTAGCTATGGGCCGCGGTATTACAGGTGGTAATGGCATA
CTAGCTGACGATTATGATATTGCACGTTTCTTCTCTGATGCAGAAGCGATTTACACGTAC
GAAGGTACACATGAAATTAATGCCTTAGTAATTGGACGCGCTTTGACTGGAGATTCTGCT
TTCGTATAAATAGCAAATAATTATATGAGATGCATTAATTTCACTAAAAAAGACTTATTT
TAAGCATAAAGCTTTTTCCTTAAATAAGAGGCTAAGATGACTGTCAAAGATACTTAATTA
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TGGACAAAAACGATCCAAATCTCATTGCGAAAAAATCTTACGATAAAATTACAGATAAGA
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GCACGCAAACAATGAATGATATTATGTATCGCGCCGAGCAACACAAGATAAGCATTGTAG
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ATGAATTTAATAAAGACTTAGTGCATAACCTTGATACCATATTCAATGCGCAAGACGAAG
CGGGACTATTTTTATGGGAGACATTACGTAATAATTTCTATTACTCTGCTATCAATGTAC
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AAGATGAGACCATTGAATATGCAACACCTATTTCTCACTTCGTAAAAGATGAACTTTGGG
ATAAAGGTGATGCCAAACTTTCCGTAACTCATGATGATCAACTGTTACTGAAATTACAAA
GTAAAAATAATGTCATTACCGATGAATTCAACGATGCGTTAGTTGATGCGATTGATTTAC
TGGAAAATGACCATTACACAAGTATGGTTATTTATGCAGATGGTAACAATTTCAGTGTGG
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TCAATACAGCACAACGTGTCGAAGTTGCGCTCAAACGTGCGAAATATGAAGCAGAAACAA
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CAAAGTATTACAAGGCGTATTGAAACGTATTGACGGAAAATTCAATAAGAATATGATTGA
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TGCTGAAAATGTAGCATCCCAATTTGACGTATCACGCGAAGATCAAGATGCTTATGCTGT
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CAGCATCTCTATATTTAACATATTTAGGTGTTTTGTTAAATTGCGGTCTCGGACCATATT
GAGAAGCTTCTGTTGTTTCAGTTGCTTGAGGTTTAACTTCAATATCACTTGATTCTCCTT
GAGTACCTTTTAACGTTGATTCAGTACCTTGTGGTTTTATTTCAAGTTTAGATGAGCTAC
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LOCUS 21 (G3)
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LOCUS 22 (I19)
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LOCUS 24(L10)
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LOCUS25(HA4)
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LOCUS 26 (L19):

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LOCUS 27A(A2)
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LOCUS 27C(A7)

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LOCUS 27D(AF7)
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LOCUS 28(H130)
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LOCUS 29(A)N10

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ACTAACC

LOCUS 29(B)GE2

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LOCUS 30 (N15)
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LOCUS 31
ACGATGGTGTCTTGCAACATCGAAAATAATGTTGTGTAAGAACGTTGTTCTACCATATCC
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LOCUS 32A(HE9)

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TGTTAATTCATTAATCGGATC
LOCUS 32B (P9)

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LOCUS 33(O14)

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LOCUS 34 (O18)
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LOCUS 35A(P13)
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LOCUS 35B (P15)
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TGGTTTATTAAATACAGCTGCATTGTTATTGAAGTATGATGATACAGCAGACCAAGAAAC
TGTTGAGAAAAATAATTACATTAAAGAACACGGTTTAAAAGCGTTTTTAAGTGAATATGC
TAAAGTTGACGATGGCTTAGCCGATGAAATAATTGAAGCGTACAATTCACTTTCATAATT
TATTGAGCTTTGTTTGAAACAAGAAGTTTCCAACGTTATTCGTTAACAATCAGTAATAAT
GTAGTAGTTCCCTTGAATTAACAATATTAAATTTCTGAACATAAAAAATACTCCCTTCAA
CATAGACACTTAACTTGTGTTATGTATGAAAGGAGTATTTTTGCGTTAATAATTTGTTTT
ATTTTCGAGCCACAGCCACCTATTCAATGGCTATTGGTCATTACTAAAACAAATTCATAT
TAACTGTTAGACTTGGTTACTTAGTAAGGAATATTTCCCTATGAAATAACTAGATGTTCA
CATTCTTGAATAAATTTTATTCTTCAGTTTGTTGGTCTTTCTTAGTGAATCTTCTAATTA
AGAATGCCATACCTGCACCTAGAGCTAATTCAGCATATGGTAAATCGTCATTATGTGACA
TACCAGTATCTGGTAAAGTTTTAGCTTGTTGTTTAGCTTTATTAACTTTTCCTTGTTGAG
CTGATTTTGTCTTAGCTTGGTGGTCGTCAGTGTTAGTTACATTAAGCATATCTTGATTAG
CACTATTGCTTCCATTTGAAACTGTAGCTGGAGATGCATTGGCACCGTCGTTTTGCGTAG
CTTTATTGTTTGCAGCTGAACCAACTGATTTTTGCGTATCATTAGTATCTGCTGTTGCCG
TATCATCTTTTTGGCTAACATTAGTTGAAGTCATTTTTTCTTTTGCTTCAGAAGATGCAG
ATGTTGATGGTTTATTCGAAACTTCAGTATCAGCTTTGCTTGGCGATTTATCTGCTTCGT
TAGATGCAACGTTAGTTTCAGACTTAAGTTGTCCTGCATCAGTTTGATTTGTCGTACTTT
CTTCTTTATCTTTTGATGTATTAGAAGGTACATTTGGTTCTGTTATGTCTGCTGAAGGCA
ATGTTTCAGTTGTTGATTCAACCATACTTTGATTTGTTGAATCACTACCATCTTTTTCTG
CCTTAGCTTTATTTTCAGATTTTGGTTGTGCAACCTTGTCATTAGTTGATTGAGATTCAG
CACTATTATTTACTTCAGCATTTTGTTTTGAATCATTTACAGATGCATTATCTTTGCTAT
CAGCAGATGATGCTGCTTCTGTGCTCGCAGTTGTTGGAGCCGTTGCTGTTGATCCTGTTG
GTGCATTCTCGTTTGTTGCTGTAGTTGTACTATTGTTATTTGTTGTGCTTTCTGCTGGCG
TTGCATTATCAGTTTCTGTTACAGGTTTATCAGTTGTGCCGTTATTAGTTGATTCTACTT
CTGGTTTACTAGTTACATCGTTATCCATTGTCGGACTGTTTGTTGATGCATCTACACTAG
AATTGTTATTAGCTTGCGGTTTATCATTTGCATCATCAGTTGCTGATGTTGCTGTTGTTT
CACCTGTTGCCGCATCACTATTATTTGGTGTTGTCGGAGAAGCGTCTGCTTTGCCATTAG
CTGTCGTCTCAGATACGTTAGGTTGTCCAGTATTTTCTGGTGTTGCATTAGCATTTGAAT
TTGCTGTTGCATCATTATTATCTATACCATTATTAGTATCATTAGCATCTGGATCATTCT
GAGGCACAATCGCTTCAATTGCAGGTATCGTTACATTTTGTAATTCAGCAACTTCTGCAT

TTGTTTGTGTTTTATCTAATTTATCAGCAAATCTGTCAAAATATCTACCTAAATCCGTAC
GTGCAATTTCTTTCGCCGATGCATCTGCATCTGCATTTTTAATTATTTCTATTTGCTTGT
TAACCACTTCTCTGATTGCTTCCAAAGCATTTTTCTTAACTTCAGGATTAATACGTTGTG
CTTTAAGTTGTTCAAGCGCACTATTTTTGACAGTAGCGATTTCTGCATTTGTAGTTTGAT
CAGAAATATCTTCAGTTGCTTTTGATAAAATGTCTTCTAAAGCATTCGTAAACGCTTCTT
TTTCTTCAGTTGTAGCATCAGCGTTGACATTTACACCTGCTTCAATCTGGTCTAGTGCAG
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CTTGTTTAGCTTGATCTGTAATTTGTTTAATCATTGCTAATGCTTCAGTTTTTTCTTCAG
CAGTTAACTGGTCACTTTGATCAATAGATTCTTTCGTATCTTCTGCTTTAACTTCAATAG
CTTGGTTCGCTTTAGGTTTAACAGTAGCATCTACTTGAATAGCATCAATTGCTGCTTTAC
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CAGTTTGAACATTTTGGTCAACTTGCTTAATTGCTTGTTGCTTTTCATCTTGTGTTGCAT
TAGTGTCAGCTGAAATATTATTTTTCTTCTGATCTGCATAAGCATATAAATCTGTTGTAG
CTGATTCTTTTTTACCTGTTGGAATTGTGTAATCGTTAATATTATCTAAGTCATTATGAA
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TTAATTCAGCAAGTTTTTGTTTCGCTTCAGCAATTTCACTTGAAGTCGATGCGTTAGAGT
TATCCGCTTCGTTTACTTTAGCATTATATGCATCTTCAATTTTAGCTAAAGCATCTTTTT
TGTACTCACTAAATGTTTTAACTGCATTAATTTTAGCTTTTCCTTCTTTAACTGCATTAT
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CAACTTCTTGTTTTGCATCATTAATTTCTTGTTGTGATGCATTTGGTGTTTGTTCTATTT
GTGTTTTCTTATCAGCTGCAGCTTGATCTAATTCTTTTTTACCTGCTGGTTTCTTAACAG
GATTTGCATGAAGTTGTTGAACTTTTTGTACTGCTGTATCTTTAGCAGTAGTTACATCAC
CTGTAGTAGTTGCTGCATTAATATTATTTAAACCTTCTTCATATGCTGCTCTAACTGGTC
CAATATCGTTACCTTTTTCTTCATTAGTAGTCTCATTATTATTAAGTATTTCAGTTATTT
TATTTTGCATTTCAGTTAGCAATTCCGCTCTTGCATTCGTTTTAACATCTGTTGATGCTT
GAATTGGGTCAATTGCTTGAATTGCATTATCTTTTGCAGTGTTTACATCATCGATTGACT
GTGCATTTTCAATATTTTGATTACCTTGTGTTAATTGTGCGTCTACTTGTTGATTTGCTT
GTTCTTTTTCTTCAGTAGTCGCATCTGCAGTTTGTGCAATAAGCGCTTTTTGTTCGTTTG
CTTTTGTTGCTAATTCATCTTTCGCAACATCTTTAATTGTTGTATCTGCAGTAATACCTT
GAATATCAGCAACTGCTTGATCTTTAATTTGCGTAACATCATTAGTTGTTTGTGCATTTA
AGATATCTTGATACGCTTTTTCTTTAGCTTTTAAAACTAAATCTTTTGCTGCATTTTTCT
CTTCAGTTGTAGCACCAGTTGTATTATCAATTGCTTGATTTTGAGTTGTCACAGCTTGAT
CAACATCATTTTTAGCATTTGATTTAACCGCTGTTGCTGGTTGCGTGCTTTGAATTGAAT
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TTTTCGCGTCTGTAACTGCTGTTGCTAATTGTTGAATAGCTGCTTCTTTTTCTTCTGTTG
TAGCGTTCTGATCATTATTGATAACATTTGTTTGCGTTGCTTGTAATTGATCAATTTCAT
CTTTAGCCGCTTGTTTCTTCACAACTTTTGGTGTTACCGCATTAATCGCTGCTTCTGCAT
TTGCTTTAGCTTCATCAACTTGTGCGTTAGTAGTTGCTGCTGAAATGGCTTGATTTGCTT
TACCATTTTCAGTATTTGCTTCAGCATCAGCTGCTTGTTTTTCTTCATCTGTTGCATCTG
GCGTAGCTTGAATCTCTTGCAATTTGTTATTTAAAATTGCTGTGATTTCATTACGTGCAG
TTGCTTTTTTATTAACTGTTGGTGTTACTTGATCAATACTATTTTCACCTGTCGTTTTCG
CTTGGTCTACATCATTTTGACTATTAGCAGCTTCAATGTTGCTATTTGCTTGTGTCACAG
CATTATCTACGTCCGCATTAGCCGCTGCAATTTCTTCAGCAGTAATGTCTTGCGTTTGAG
CGATTGCTGTTTTACGTTCATTCGCTTTCGTAGCAATTGCTTCTTTCGCATTATCTTTAG
TTGTTGTTGCTGGCTGAATCGCTTCAATTTTAGCAATTGCTGCTTTTTTAGCCGCTTCAA
CTTCCGCATTTGTATGTGCTGCATCTATTGCGGCATCAGCTGTTGTTTTTTCAGTTTGAA
CTTGTTGTTTAGCAGCTGCTTTTTCTTCAGTTGTTGAGCCGTTATTTCCATCAATTGCTG
TTTCTTGAGCTTGTACTTTATCTGCAATTGCTTGTTTTGCTGCTGGTTTAACATTTGCAT
CAGGTGTAATGGCTGCGATTGTAGCTTCATTTGTAGTTTTTGCATTATCCACATCATTGT
TTGCTGCAGCATTATCTATATCAGCGTTTGCAGTAACTACTGCTT
LOCUS 36(P5)

GATCATCTCTATCAATTTTTATATTAAATTCATTTTTTTGAATCGATAAAATAAACTCGA
TTAGCTCTTCCTTATAAGACCTATTATATTCAATTATGTTTATAGCCATTTTTATCTCCT
TTTTCATTTAATTTAATTATAAAATGTGCGTTTAGTTTGTATCTAGTGTACTCAGTACAG
CCTCAAATGAAGTTTCATTCCACTTGGCACTTAATAAAGACAAGTATTTTAGCAGTAATA
CAATAAAGTCCAATAAATTTCCCTAACTTCAATATCCACTTTTTAAAAAATGTATTTTTA
ATTAATAAAAAAACTCTCCCCAATTTCTATGGGAAGAGCTATATATTTAATGTCTAAACA
TTACTTTTATTTATTATGAAGGAATTAGAATCCCCAAGCACCTAAACCTTGTGCTTTGTA
TGCTTTAACAGCTGCGTTGATTTGTTGGTCAACAGTGTTTGTTGGACCCCAACCTGGCAT
AGTTTGGAATAAACCTGAAGCACCTGATGGGTTGTAAGCATTTACTTGACCATTTGATTC
ACGAGCGATGATTGCAGCCCATGTAGAAGCTGAAACACCAGTACGTTGAGCCATGATTTG
AGCTGCTGATGAACCAGTAGCACCTGCAGTATTACCATTGCTTAATCTCACTGAACTTGA
AGTAGTTGAAGTGCTGTAGTTATGGTAAGTTGGAGCTGAAACAGCTTCAACGTTTGAGTT
ACTTGATTGTGCATTGTAGCTTACTGATTGTACATTTGAACCTTGGTTGTATGAAGTAGT
GTAGTCTGCACCTGCAACGTTTGAGAAACCAGCAGTTTGACCATTAGCTGCTTCATAGCT
CCATGACCATGTAGTACCATTTGAAGTGAAGTTATATTGGAAACCATCTTTTACAAAGTG
GATGTCATATGCACCATCTTTGATTGGAGCTGCATTTAATTGATCTTGGTGATTATGCGC
TAAGTCAACTAAGTGTGCTTGATCAACGTTTACTTCAGCAGCGTGTGCTTGATGTCCTGT
ACCTGCTGCGTAACCTGTTACACCTAATGCCACTGCTAATGATGATGCCATAATTGTCTT
TTTCATAGTAAAAAATCCTCCAGTAATAATTGTAAGTTTATGTTTTTAGTAATTATATTT
TGAATTTGAATGTCGTAGTGCAAGTTTAAATTGTCTTTTATTTCTTTCAACGGTACTCAC
TATATCACAAAAAACCAGCCAGTAAATTACACTTTCTTTACAAAACATTACAATATCAAG
TGTTATTTGTAATGTTGAAATATGGCTGTTTTATACTGTAATGTGAAATATGTGCCCTTT
AGAATCCAATCAACCCTTGAAATAGTCTTTAACACATAAGATTTTTACTATATTTAGCTC
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TGACATGTAACTTCTCTTATTTTCGTACATTAAACGCAATTAAAAAGCAATCAACAAATA
TGTTTCTACACATGTATTGATTGCTATTATTGTTGTATATTCAAAGTTTTAAAACACACA
TCTTTTGTGAATTGTCTTATCTTTTATTAGCGCAAATAAACTGCAGCTCAATTATATTGT
TCAACTTCATTCTCGCAATTCACAATAACATTAAATAATTTTTGGTCTCATATTTTCAAA
AAACATACTGTTATTATCCCATGAATTTAAAAATATCATTAGTATATAAACGAAACACTT
TACGATAAATGATATCTGCAAGCCAAGCTGTTACAAATGGTACAACAAAGAACGCTACTA
CAATTAGTAAGACACTCAACCAAGCAGAATCAACCTCCATAAATTTAAATGCATTAATCG
GTCCTACCATTCCTATAAAACCAAATCCAGCTGACTCTTTCGTTCCATGAATACCTACTA
ATGCTGATACCAAACCTGATACAATGGCTGTCGTTAATATTGGTAACATAAGAATTGGAT
ATTTCACCATATTAGGTATCATCATTTTAACGCCTCCAAAGAAGACGGATAACGGCACCC
CTAAACGATTCACTTTACTTGTACCAATTATCAATACTGCTTCAGTCGCGGAGATACCAA
TTGACGCTGATC

LOCUS 37(P8)

GATCTGGCGTTGGTTCTGGTTCTGGGTCTGGACTTGGTTCTGGGTCAACCGGCGGCCCTG
GAGTTGGGTCTTTCGGATTTACTGCTGAATCACCATCAGCACTTCCACCACCATAACGTA
CAACATTCTCATTATTCCAACCGAAAATACTGTAGTCTCTATTTGTTACAGGATCAACAT
TTTCTTGAATAACCTGAGTTTTTAAGTTCTTACCTGTATTGTCGTAATGCCCTTCTACTA
ATACTACATATGTTTTAGTAATATCACCAAATTTAATACTAGCTACATTTGGATGCTCAT
AATAGATTCTATTTTTAAATTGGTCTGTTACTTCTTTAAGGTTAGAGTCATTTGGATCTG
CATAGTAGCTATCTGATAATTTAGATGTATCATTCACTTCAAAAATTCTCAGTTTTGTAT
CTGTAGCACTTACTTTACCGCTACTTTCTTCGATTTTATCTTGGTAGCCTTTAATATACA
CCCACGTATTACCTAAAACTCGTTGCTTAGGGTTAACAAATACTGTTTGCTTGTATGTGT
TTTGACCTGAAGCTGTATCTACACCAATAATTTGAGAAGAAATGTTCGCGCCATTTGGTT
TATCAATTCCTGCAATTGGCGAACTATAGTTATAAGTAATTTTATTATTAAACATTTCAT
CCGCAATATTAATATTCGCATCATATGTTCCTGATTTAGGTGCCTTTGCTCGGTCTGTAA
ATAAAGGTAATGAAAATTGTCCGTTAATATTTTCTTTATTATTTACATAATCTGTAAAGA
CAAATGTATACGTCTTAGTCAAGATATCATATGTTGCTTTAGCTACAACATCGCCATTCG
TACTTTTAATGTCTGCAATTGGCATCGTATTATTTGAATTAGAATAATCCACGTCTCCAT

TACCAGTTAAACTATCTGGTAACTTCGCTGTAAAATAATCCCCTGATTTCACTTTATCTG
TCACTGTAAAATTTGCCGCCATAAATGTGTTACCACTTTGATTAGGGTCAAATGTAGTCT
TTTCTAACTTGAAATTACTTGCCGTAACTTTATCATTTACATTTGTACCTTTAGCATCAG
CAGCATTTACTACCGGTTCAGCAACAGCTAAACTACGTACAGCTCTCGTTCTAACACTTG
GTTTACTAGTTCCTTGCGCATTGGAAATCGTTTGTGGTGATGATTGTGGTAAATCTAATG
TTTGAGAATTTTTAAGCTCACTGTTTGTTGCTATGCTATTAGCATCATTCGTTGTTTTAT
TATCTACTTGAGAATTTGCTTCTTGAGGAACAGTTTGATCTTGCATTTTTGCAGCAGTTG
CTTGATTTTTAATTGCCGTCGGTTGAGGTGTTTCATTTGTTGAAGCTGGCTCTGTTGTAG
TGGTATTGCTCGTTTGTGTAGACATTGGTTTTGTTGTGCTATCTACATTCGCACTGTTTG
TGTTTGCACTAATATCAGATGTATCATTAGCCGTTGTATTTAATTGAGGTGTTTCTATCA
TATTGTTTTTTTCGGAATCTGCACTTGCATTATTTTTCGAAGATTGCGTTGTATCGTTCG
ATTGTTCTGAAGCTTGTGCTTGATGATTGCCTATCCCAAATAGTATAGTTGCCCCTACTA
TTACTGATGTGGTACCTACTGTAAAACGTCTAATCGAATACTTATTCTGCTTATTCGACA
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TTCTTCCTATTTATATAACTTAAAATTTTCTGTTAACTAGCAAAAATCAATATACTATTT
TTACACTATTACAAATTTTTTACTTTTCAAAAACTTAGAAGTTCTAAATTTTTCATCACC
TTAAATTTTACTGTAATTTCAACAATCAAATTTAACTAACATTTTAAATTATTCATCATG
CTAGCAAAAAAGGCCTAACGTATAAATGTACGTTAGACCTCATGTTCAACTTATTCATTT
TACATTGTATATTAAACACATACATCATTGAATAAATGTTTGCTTACTAACCAATTTTTA
TGATC

LOCUS 38 (P16)

GATCAGCTAACGCTACAAAACTAATAACAAATGCGATGATGATTAATACTAATTTACCTG
CTGCTAATACAGAATCTCCAAGGAATGAGAAGAATGGTTGACGTTCAACTTCATTGTTTT
TAAGACTGTAAATAATATCTTCTTTCTCTTCAACACTTACTGGATTCAACAAGCATGACA
CAATAATCGCGTTAACGATATTTAGTGGAATTGCCGTTAGTACCAGTTCTCCTGGTACCA
TTTGTACATACGCACCTACAATAGCTCCCGATACAGAGCTCATTGACATCATTGCGATTG
TTAATACACGCATTTCATTCATACGTTTTAGTTGCTCACTTGATACGGCTAATGCTTCAG
TATTTCCTAAGAACATCATTTCTATCCCAAAGAATGACTCGAATTTAGGTTGTCTTGTTA
CTTTAGCTAGTAACCAACCAATACCTCCAATAATTTTCGGTAAAATATTAAAGTACATTA
AGATATCAAATAATGGCACTATTAATAATATTGGGAATAAGGCTGCAACAGCCATATCCA
TCATTTTAACATTTGTCAAACTTGCAAATGCAAAACCTGTACCAGCATGCGCTGACTGAA
CTACCCAAGCGATACCATTGGCTGCTCCTCTTACTGCTTTTTGACCCCAATCAAAATAAA
TAAAGAACCATGCTAAAAACAGGTTTAAAACAACTAAGATC

LOCUS 39 (HB3)

GATCTTTCGAAATTGTTTCTTCAAAAGTTTTTGGATGAAAAGTTAATTTTTCTGGAAAAC
ATAACTGTTGTGCCATATATCCAAAACTTTCTTGATATTTTTTAAAATTATCGAAATTAA
TCACGGAAAATCCCTCCATAGAAATTCTCATTATAAATTTCTTGACCAGTTTTCCCTGAA
CCTACTGCAACGCCACAGCCTTCACAGTTATCTCCAAAATGCTCGCCGCCGTAATTGTAT
CCTGTACTACCTTGTGCGTGATACGTATCTAAATAGGTTTCTTTGTGTGATGTTGGAATA
ACAAATCGATCTTCATATTTGGCTAGTCCTAATAAACGATACATGTCTTTAGTTTGGCGC
TCGGTTATACCTAATCGCTCTAATCGAGACGTGTCAAATGGCTGTTGAGTAACTTGAGAT
CTCATATAACTTCTCATCATTGCCATACGTTGTAGGGCTCCTTTTACTGGCTCTGTATCT
CCTGCAGTGAAAATATTAGCTAAGTATTCAATAGGTAAACGCATTTCTTCAATGGCTGGG
AAAATCGCATCTGGATTTTGAGTTGTATTTTTACCTTCAAAATAGCTCATAATTGGGCTA
AGTGGTGGGCAATACCAAACCATCGGCATCGTTCTAAATTCAGGATGTAACGGAAATGCA
AGTTTATATTCAATTGCTAACTTATAAATTGGAGAGTTTTGTGCAGCTTCAATCCAATCG
TAACCAATACCATCTTTTTCAGCTTGAGCAATGACTTCTTCGTCAAATGGGTTTAAGAAT
ATATCTAATTGTTTTTCATATAAATCTTTCTCGTCTACTGCTGAAGCTGCTTCATGAACT

CGATCTGCATCATATAATAAAACACCTAAGTAACGCATACGTCCTGTACAAGTTTCAGAG
CATACCGTAGGCATACCCGCCTCGATTCTCGGGAAACAGAAAGTACACTTTTCAGCTTTG
.TTCGTTTTCCAATTGAAGTAAACTTTCTTATATGGACAACCTGTCATACAGTAACGCCAT
CCACGACATGCGTCTTGGTCAACTAATACAATGCCATCTTCATCACGTTTATACATAGCA
CCTGAAGGACACGATGCAACGCAACTTGGATTCAAGCAATGTTCACATAAACGTGGTAAA
TACATCATAAAAGTTTCGTCAAATTGGAATTTAATATCTTCTTCTATTTTTTGGATGTTA
GGATCTTTTGGACCTGTAACATGACCACCTGCTAAGTCATCTTCCCAGTTAGGTCCCCAT
TCAATTTCAATGTTATCCCCCGTAATTTCTGAATACGCTCTAGCAACTGGCGAATGCTTC
CCTGATTTCGCAGTTGTTAAATGTTCATAATTATAGTTCCATGGCTCATAATAATCTTTA
ATTAATGGCATATCTGGGTTATAAAAAATTTTACCTAAAGCAATTTTTGAAATTCTACTT
CCAGATTTTAATTCAAGTTTCCCTTTACGATTTAGTACCCAACCACCTTTGTAGTGTTCT
TGGTCTTCCCAACGTTTCGGATACCCTACACCTGGCTTCGTTTCTACGTTGTTGAACCAC
ATGTACTCAGCACCTGGACGATTTGTCCAAGTGTTTTTACATGTCACACTACACGTATGG
CATCCTATGCATTTATCTAAATTTAATACCATCGCAACTTGCGCTTTAATCTTCAAGCCA
ATTAACCTCCTTCATCTTTCTAACTGCTACATATAAATCCCTTTGGTTCCCAATTGGTCC
ATAATAATTAAAGTGATAACTAATTTGTGCGTATCCTCCGACTAGTTGTGTTGGTTTCAA
ATGGATTCTAGTCGGCGCGTTGTGTGAACCACCACGTGTATCTGTAATTTCTGACCCAGG
CGTTTGAATATGTTTATCTTGTGCATGATACATAAACATTGTACCTTTAGGCATACGATG
CGAAATAACTGCTCTTGCCGTTACAACACCATTACGGTTATACACTTCTAGCCAATCATT
ATCTTGGATATCGTGTTTTTCAGCATCTTCATTTGATATCCAAACCGTTGGACCACCTCT
AAATAGTGTCAACATATGCTTATTATCTTGATACATTGAGTGTATATTCCATTTTCCATG
AGGCGTTAAATAACGCAGTACCAAAGCATCTGTACCACCTTTAATTTTCTTATCTCTATT
CCCAAATACCATTGGCGGCAATGTCGGTTTATATACTGGTAAGCTCTCCCCAAATTGTTG
GAAAACTTCGTGATC

LOCUS 40 (HB5)

GATTCATCAATACTTTTGAAACACCACCTAATGATGCAATGTCTTGTTGGGAGTCACCTA
AGTGTCCGGAATGATAGATAACAATATTACCTGTTTCACGTTTTAAAATAAAAGATTTAA
ATAGAAATCGATTATCAAAAGGCAGTTCCGAAGTAGGTGTCGCATATAAGTTTTTTGTGA
TGGATTCTAAACTGTCATGTAATTTGGACTGTTTATTTTTAAATTGATTAGTCATTTTAT
TTCATCCTTCGATTAATTTGAATTGTACATACGCAGTACCCTTTATTTAATTTAATAATC
AATGAGAGTCTTTCAAACTTCGATTTAGAATATGCTTCATACAATAAATAAGTACTTGGA
GCACTAAAAAATTAAATCTTTTAGTACAACATTAATGAAAACCTAAAAGTTCATCCTACA
ATGCTACTAAAAAAAGGGGAATGGAACAGAAATGATATTTTCACAAAATTCATTTCGTCG
TCCCAGACCCGCTTTGAATTATAAATTATCGTCTTGTTCTTCTTCTGATACTTGAACGAT
TCGCAATGAACGACGTTCAACTTCTTTTAATTTTTCAGCACGCGTTTCAAGTTTAATTCT
ATCGCGCCCTAAAATGATTAAAAATGATATCATCATGAAAATAAAAATAACAATTAATGG
CACACTTGCCAGTATTGAAGCAGTTTTCAATACTTCTAATGCACGTTCACCACCAACTAG
CATCAATGAAAATGGCAATAAGCACAATGCAAATGCCCAGAATAAACGATTGGCACGTAA
TGGTTCGCCTACCACTTTTTTCTGAGATGCTGCCGCTAAAATATATGAACCCGAATCAAA
TGTTGTTGCTAAGAATAAGAAAGCAGATACTAAGAATAGTACAATCATCAATGATGGGAA
TGGTAAATGATGCACCACTTCAATAATGGTTGCCTCTGTACCATGTGTATTTAAATATTG
TGTTACATTAAACTGTCCAGAAATTTGTAAATACACAGCATAGTTACCAAAAATACCAAA
GAATAATACGCATCCAAGCGTTCCATAAATAATTGTTCCTAGCACGACTTCTTTAAGGCG
TCGACCTTTTGAAATTCTAGCGATAAATAAACCGATAAATGGCGCATATACTAACCACCA
TGACCAGTAGAATATTGTCCAGTCTTGTGGGAAATTCGTTTCTTTTCGACCTTTAATACC
ACCGAATGGTTCTAACCATGTTGCCATATGAAAGAAATCTCTCAACATATTTCCGAACCC
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TACAAAGGATAGCCAAACGTTGATATCACTTAACTTTTGAATACCTTTTTTCAATCCTGT
ATATGAACTAATGGCAAATATAACCGTGATTGTTAATAAAATGGCCGAACGTAAAATCAT
ATTTTTACCATCTAAACCAGTTAATCTTTCTATGCCTGCAGAAATTAATGGCACACCTAA
CGCTAGTGATGTTGCCGCACCACCTAGCAATCCAAAGATAAATAAGATATCTACAACTTT

ACCTACAAATTTATCTGTTTGACCTTTTAAAATCGGACGACAAGCTTGACTAATTTTATA
CACCGGTTGTTTTTTAACAAATACTAAATAACCAATTGGTAATGCTGGTAGAACATAAAT
AGCCCAAGCAATTGGCCCCCAGTGGAACATACCATATTGCGTCGCATATTGGAGTGCTTC
ATCACTCATACTTTTCGCGCCATTTGGTGGAACTTGATAGTAAAAAGCCCATTCAATAAC
GCCCCAGTATAAAATATCAGAGCCTATGCCTGCACAAAACAGCATTGCCGCCCATGTAAA
TGTATTAAATTCTGGTTTATCACTTGCTTTACCAAGTGTGACATTACCATATTTACCAAA
TGCGATATACATTACAAAGCAAAAAATCGCCAGCCCCATAAATAAATATATCGAACCAAT
TGAATCAGAAATGGCACTATTAATACCAGTGATGATATCTTCACTTGCTTTTGGAAAAGC
CATCATAGGTATAACTGCAAAAAGAAGTACAGCTACTGTCCCTATAAAGGTCGTCCAGTC
CATAACTTTCTCTTTTTTCAATTGTGCTCCCCCTAATTATTAATTTTATGAATCCTGTTT
CGATTTATCTCAAAATGTAATAATTATATTGATTCACAAAATTGACAATAACTAACATTT
AATAATAATGCAAATTTCATACAATTTGAAACTTGGCAATTATTGAATATTTATATAATT
TTTCCCGTAATAAACAAAACCTTAATAGCGCTAAAATAACAGTGTTAAGTTACGATTTAA
CGAATTTAACAAATTTTACTAGAATGGCATTTAAGAATATTTATACGTTATTAACGAATA
TTTATTTATTGTAAAACGCTACCAAAAAGTTAGACTTCCTTCCCACTAAAATACCACTTT
TCTCTTTCAACTTTTTTAAAAAACGGATATGCAACTTTTAGTATTGGTATCAAAATGATT
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TGTACCTAACCTAAAAAGAAGCCAAGGCAACGAATGTTACCTTGACTTCTAATACATATT
CAACTAACTATATATTCAATCATACGCGCATGCGAGAGTGATTGTTGTACATCTATAATG
CGTTGATTTAAAGAACCTTTATATGGTAAATCAGGTTTGAATAAGTGTTGTATAAATAGA
CCATCTACTAAAACGTCAATGTATGATAATAACTCTCGACGTTCTGTACAATCATTTGCT
AAATATTCATATAAAAATCCAGTCCATACCCAAATTGTCTTTGTATTTCCAAAACGTGCT
CGAAATGCTTTGACAAGATTTAATGTAATATCCAAATTACAAAATGGTTCGCCACCTAAT
AGACTTAGCCCAGATATATAATCATGATCGCAATCATCTAATATTTCTGCTAATATTTCA
TCAGTGTATTTCTCGCCATATCTGAACTTTTGTGAGGCTTTGTTATAACATCCAACACAA
TTAAATGGACATCCTGATACATAAACACTGCATCTTACTCCTTCACCGTCAACAAAGCTA
TTTGATTCTATTTTAGCAATATAACCTTGTCCTTGTTTAATGTCTAAAAGTATCATTCTT
TAGGCGCTTTCATATGTTTTACTCGTGCGCAAATTTCTTTATGACGGCCTTTAATTACTG
GACGTTGAACTGGATTGCCTAGGTAACCACATGTTCGTTTAACGACATCAACTGTTTTAG
GATTATCATTGCCACAGTTCGGGCATTTAAATCCTTTTTCAGTTGCTTCAAAATCTCCAT
CGTAATCACATTCATAACAATGATC
LOCUS 41 (HB7)
GATCTACATTATATTGCTCAAATAAAGGCGATAATACTTTAGGATTTGGCTTCTCATAGG
CATCCGCTTCGGTAGAAATGATCAAATCGAACAACGAGGTAGCATTGGTATGTGCTAAAA
ATTGTTCTACACCTTTTTTAGTATCACTCGTAACAATACCAAGTTGATAGCCTTTTGCTT
TCAAATCGATAAGTGCTTCTTTAACACCTTCTACCCAATTAATTTCAGGAATACGTTCAT
CTACCAGCTTTTGACTTGTTGACTTGGACCAGTCGGTTGTATCTTGTCCCGTCACATCAT
TAAATGCCTGGATAATTTGTTGTAAAGATCCTGAACCCATCACTGATTTTGGATCAATAG
ATTCTTTAATGACACCGAGTTGTCTTAAAGCAGCTTCTTTATTATGTACTGGGAAAGTCT
CAAGCAATGATTGTACAAATCGTACCCCTATTTTTTCCCAACTTCTATCAAATTCAATTA
ACGTACCATCTTTATCAAATAATATCCATTCCATTGATATCAATACTCCTATTTATTTAT
TTCGTATTATGCTGATTCTATGATATTCGTTATCCCCTGAAAATGAACTCGTAGTATTGT
TCTATTTAAATATTGAATTAAATATAATAATAAGTGAAATCCCCTTCAATACTTAACAAT
AAACATTGTAAACTTAATTTATTACCATGCTTCGCTTCATTGAAAGGGATTTTAGTCATG
ATTAACTTTTGCATATTGTTTTCATGATTATATTCAATTTTTATTAATATTTTGGTACAA
CGACTCTCCAACCATTTTTATCTTCTAAAGTACCATTTTGAATACCAGTATAGACGTCGT
ATAATTTTTGAGTAATTTCACCAGTCTCATTATTATTAATAACGATTTCACGATCTTCGT
ATCTCAATGTACCCACAGGTGAAATAACTGCTGCAGTACCACTACCAAATACTTCTGTTA
ACTCACCTTTATCATATGATTCGAATAATTCATCGATTGAAACGCGGCGCTCTTCGACTT
CATATCCTAAGTTTTTAGCTAATTCGATAATAGATTTACGTGTAATACCAGGTAAAATAC
TGCCATTCAACTCTGGTGTAATTACTTTGCCATTTTCAACGAAGAAAATGTTCATGCTAC

CAACTTCTTCGATATATTTCTGTTCAACACCATCAAGCCATAATACTTGGTCATAACCTA
ATTTATTTGCATTAGTTTGTGCTAATAAACTTGCCGCATAGTTACCTGCAACTTTTGCAA
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TTAAAGTTTCACCACCATAATATGCACCTGAAGGAGATAAAATAATTAATAATTTATACT
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ATGATTGACCTTCCCCTTCAGGAATCCAATCTCTTTCAATATCAACTAATTGTTTTAGCC
CCTCTAACAATTCTGCTTCGTCTACTTGAGGCATTTCTAATCGTGCTAACGAGTTATTAA
GACGCTTAAAATTTTCTTCAGGACGGAAAAGTGCAACTTCCCCATCTCTTTTATATGCTT
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TAGGACCATAAGGTACTATCTTCAAATCATGCCATCCTTTATCTGCATCATAATCATAAC
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CGTATTAATTTCACAGAGACAAGTAATCTGTGTTTTACTAATATACTTTACATACAAAAA
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GTGAATGGAAATGATTAGTTATTATTTTTAACAGTATCTTTTTGTTCAATAGCTTCTAAC
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LOCUS 42 (HB8)
ACGGACTAATATTTCAACTTCCACATTAAAGACACGTTTAATCAACGAATAAATACGTCT
TGCCGTTGTTGCATTTTCCGTTTGAACATTTATAACAAATTGTTGATTTGAAAGACTAAG
TGCACCATTCATTCGAATCAGTGCACTGAGCTCTGCTTTTGCATTCATTTCATCGACGTC
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CCCCAGGTTGCGTCATCACATTAGAAACATATAGCTTAGGCGCATCAGAATGAATTAACG
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CAAGAACGATTAAATCTGCTTCCCTTAAAGCATCGATTGCTTCTTCCATTGGTTGCACAT
CGTTAGGTTCTAAAAACACACGATCAATTTTTTTATGTTTTTTAGGAATATTTGTTTCTC
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CATTCGTAATATTAGTCATACCTGCGATTAATAAATTACCTAATGAGTGACCGCTAATTT
GATTTTCTTCAAAGCGATACTGAAAAAGTTGGCTTAAAACTGACTCAGAATCACTTAAAG
CTGCAATCACATTTCTGATGTCTCCTGGTGCTGGTATATCCATTTCATCTCTGATTTTCC
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TATCATAAAATCTAACAAATCAGTTAATTTTTCAAAGAAAATCTCCGTCTCTTTCCATTT
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TCGACGAATGCGTTCTTTTAATTCTTTAGGTGATAACTTTGTAGTATCTATAACAAAATT
AGCTATACTTCTAATTTGAGACAAATGCTCTCGCTCATCATTAATTGCATTGATTAACGA

TC
LOCUS 43 (HB10)
GATCAACTCATTGCAAAATACGATTTATAGACATCAAAGAATCAATACATTGTAAAGGGG
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CTACTAGCTATGTTGTTCATTGGCGTTTATTTTACCAAGCGCGCGAGCCAAAGTACCAAT
AGTTTCTTTACCGCAAGTGGTCGCTTGCCATCTTGGGTAGTTGGCTTTTCAATTTATGCT
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TCATATATCGCTGGTAACATTGCTATCGTCGCAATTATTCCATTACTTATTTATTTCTAT
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GGCCCTAGCATACGTGTCATTGGCTCATTATTATTTGTCGTTTACCATTTAGGGCGTGTT
GCAATTGTTATCTACTTACCAACATTAGCAATCACATCTGTATCAGACATGAACCCTTAT
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TCATTTTATACACATGAAGCTGTTTTACCAAAAGGCTTCAATACATCATCTGTAGTGCCA
TATTTCATTTTGACTGAGATGCCACCATTTGTAGCAGGATTACTTATTGCAGCCATTTTC
GCCGCTGCACAGTCTACCATTTCATCTAGTTTAAATTCTATATCTGCTTGTATTTCAATC
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AAATTTATGCCTGCTTTACTA
LOCUS 44 (HD7)

TCCACTCTCTTCGTTGAATCCAAGATTAACGATTGGCAAACAAATTACAGAAGTAATATT
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LOCUS 45 (HD9)
GATCTGAAGTAGCTCGATTTTAAATAGTTTTCAGCAATGACATCGTCTTTTTTCTGTCGGC
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ACCTCACCAACACCTTCATGAATTAAAGACATTGGCAATTTCTGAGATAAGACATTCTCA
TCACGGCTACCAGTATAATATCTTTGATC
LOCUS 46 (HE9)
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TGTTAATTCATTAATCGGATC
LOCUS 47 HF6
GATCCAATTGAATTTTTCTCATTTACAACATAATCTGGATATTGAATGTTAGCAGTTGTT
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GAGTTTTGTAATCTTTATTTAATCATCATAAAAAATAGTATTATTTGCCCTTGAAATTAA
TATCTTAGCTTTTCTAATTCATAGACAATTACATTTCTGTAACAAATTAAATTGTATCTA
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TTGTCTGAGTCCGAATCGCTATCTGAATCTGAGTCGCTGTCTGAATCTGAATCGCTATCC
GAGTCTGAGTCGCTATCTGAGTCTGAGTCGCTATCTGAATCTGAATCGCTGTCTGAGTCT
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CTATCCGAATCTGAGTCGCTATCTGAGTCTGAGTCGCTATCCGAGTCTGAATCGCTGTCT
GAGTCTGAGTCGCTGTCTGAATCTGAATCGCTATCTGAGTCTGAGTCGCTGTCTGAATCG
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GAATCTGAGTCGCTATCTGATGTTTCTT

LOCUS 49 (A) B13

TCTTTATTCGAACTATTAGATTCACTTTGACCAGTAGTCGTTCCATCAGATCCTTTGTCA
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AGCAAAGTTGAAGACAATCACTCTACTAAAGTTGTAAGTACTGACACAACAAAAGATCAA

LOCUS 49 (B) K16

AGATCAAACTAAAACACAAACTGCTCATACAGTTAAAACAGCACAAACTGCTCAAGAACA

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CTATATGATGCTATCGTTAAAGTTCACGTAAAAACGATTGATTATGATGGACAATACCAT
GTCAGAATCGTTGATAAAGAAGCATTTACAAAAGCCAATACCGATAAATCTAACAAAAAA
GAACAACAAGATAACTCAGCTAAGAAGGAAGCTACTCCAGCTACGCCTAGCAAACCAACA
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LOCUS 50 (A) GB2
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LOCUS 50 (B) G10

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LOCUS 51 (GC8)
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LOCUS 52 (E1)
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LOCUS 53 (E20)
CATACTTCTATGTCTGGTTCTTGATTTAATAGCTCATAAATATCAAATGCTGGTGATTCT
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LOCUS 54 (E105)
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LOCUS 55 (E18)

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AACAAAAGTGTTAACGATGGGGTTCATAGATGATTTGCTATATCCGGATGATC

LOCUS 56 (F5)

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LOCUS 57 (F3)
GATCTTCGCGTCTTAATGGATGCCATATACGAACTGAATGACCACCAAGATTTGCGTGAG
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LOCUS 58 (G8)
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LOCUS 59 (G23)
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LOCUS 60 (G29)
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LOCUS 61A (HA7)
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LOCUS 61B (G28)
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LOCUS 62 (H3)
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LOCUS 63 (GD10)
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LOCUS 64 (F5)
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AAAGAACAATAATCAACATGGTTGAATGCATTTTTGCAGTAAAGTCAAAATAAGACATCA
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TAATGTTTGGTATATTGTTAAAATTGTGTCTAAATATAGGTGTGATTCAGATTAGTTTAT
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TGAACTTATGGACATGAATTTCGATTTATACATGAACGGTGTTGTAGAACAAGCAAGGAA
TGAAATTGAATCTGCGGGATATGAGCAATTAACTACTGCAGAAGATGTTGACAAAGTTCT
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CGCAAGACCAGCAGCATCACATGCTTTACATTATGACGTATTACCTGATCGTCTAGTGAC
AGTATTTGCTGGACAAGATAAAGAAGCGACACAAAGAGCGCGTGAATACTTCGAAGGTTA
TGCGCCTTCAAGTCCGTCATTTGCATTAGTAAAAGATGGAAAGATTACAGAAATGATTGA
AAGACATCAAATCGAAGGTCATGATGTGATGAACGTAATTAATCAATTACAAACATTATT
CAATAAATATTGTGAAGAAAGATAAGAGGCGCTAACCCATGTTAAAGTTAAATCCTTACA
AGATTGGATTTAGAACAATAAAAACAGCAGTGGGTATGACTTTAGGTGTAATTATTAGTA
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TCGTATTGTTATTTATACCATTAACTGTCGTATTAAAAGTACAAGAAGGTGTCATTACGA
GTTGCGTTATATTACTTCATGTTTTTAATGCAAAATCAATTGATGCACATTTAATTGTTA
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LOCUS 65 (F110)
AACGACCACAAAACATACACAACTACATTTTCTCTAATTATTTATATAAATATTTTATCG
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CGACCGCCTTTGATATAATAATAAAGTTCAACTGCGCGGTCATAGTTACTTCCAAAAGCA
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AAACCATGCACTAAAACGATAGGATCC
LOCUS 66 (E1)
CAGGATTCGTTTTATCTAACTCTTCCCCAAAAGCTGATAAGTGTTGTGTAGTTTGTGTTG
TCATTACAGTAACTAAGATTGCTGTACCTATAGAGCCTGCTAATTGACGCATCGTATTTA
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CATATAAATCATCTAAATTGTATGCATAAGCGATTGGGTTACCAGCTTGCACCATTGAAC
CTTCCATACCATCTAATTTGGCAATTGTACCTTTTTGAGGCATT

LOCUS 67 (F119)

GATCAAAATTTTGAATTAAATACTGTCTCAATTTAAAGTCGAGTTCTTTAAGTGAAATCT
CTTCTTTATAAATGTAGTGTACTCTACCGTACGTAGCAATACCGTCACCTTCATCTCTCT
TGATTTGAAATCTTGGTGCGTTTATATAATCATAATAAGCGTCTTGATTTTTCTTAGTGA
CACCACCATATGAAAACACTGTGCCATTACGGTTTTCCGCTTCTTTAACAACAAATATGT
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TTGTGAATTTTCTATTTTTATCAAAGATAAGGTAATGCTTGCCACCTTTGCTATAACGAT
AACCAGTAACATTTTTAAGTTCCTTACTTGCGCCACTATAGTAATCTCTTAAGTCAAAGA
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ATGACGTTATTGTTCCTGTTGCTAAAATACCTAATGCTAAACTTGCTTTCGCAATTGCTG
TCATTTTCATAGTTGTATGCTCCATTCGTAATTATTAGATTTGTTCGCTTACGTCTATTG
AATCATACAGCTTTATTATAGTTAGCGTATTTGACCTTTCACATTAAACCATGTTTAATA
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TAAGTTGTTTTCTCAATTTAAAATCAAGTTCTTTCAAGGAAATCTGTTCTTTAGTAATCT
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GCGGTGCTTCTATTTTAGTTGAGGGCGGTGTTGATTGTGGTGCTTCCACTTTAGTGGAAG
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AAAGACCATAATTATCAATAAGGTATTTTCTTAATTTAAAATCAATCTCTTTCAATGACA
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LOCUS 68 (G27)

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AATGAAACTCGTTTAACATTTCATCTGTAGTTCTAAAATGTGCTTCCGGTAAAGTTGAGC
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CAAACAAATAGTGTGCATTTCCTGTCGCAATAACAGGTATACCCGCTGTGTCACCTGCAT
GTATTAAACGTTGATAAATTTCATGTAATGTTTCAGTATCTCTAATAAGCTCTCTATCAA
TTAAATCTTGATAAAGTGCCGGTGGTTGAATTTCAATAAAATCATAATATTTGGCAATTT
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TGTTTTTGTTAGAAACATCTATACGTGTCAGTTCACCTGAATTTAA

LOCUS 69 (H110)

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LOCUS 71
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LOCUS 72
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LOCUS 73
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LOCUS 74
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LOCUS 76

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LOCUS 77
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LOCUS 78
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LOCUS 79
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LOCUS 80

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LOCUS 81
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LOCUS 83
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LOCUS 84

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LOCUS 85 (F126)

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LOCUS 86

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LOCUS 87
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LOCUS 88
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LOCUS 89
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LOCUS 92 F102
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LOCUS 93 H128
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LOCUS 94 HA2
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LOCUS 98 GE2
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TCTTGGTAGCCTTTAATATACACCCACGTATTACCTAAAACTCGTTGCTTAGGGTTAACA
AATACTGTTTGCTTGTATGTGTTTTGACCTGAAGCTGTATCTACACCAATAATTTGAGAA
GAAATGTTCGCGCCATTTGGTTTATCAATTCCTGCAATTGGCGAACTATAGTTATAAGTA
ATTTTATTATTAAACATTTCATCCGCAATATTAATATTCGCATCATATGTTCCTGATTTA
GGTGCCTTTGCTCGGTCTGTAAATAAAGGTAATGAAAATTGTCCGTTAATATTTTCTTTA
TTATTTACATAATCTGTAAAGACAAATGTATACGTCTTAGTCAAGATATCATATGTTGCT
TTAGCTACAACATCGCCATTCGTACTTTTAATGTCTGCAATTGGCATCGTATTATTTGAA
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TCCCCTGATTTCACTTTATCTGTCACTGTAAAATTTGCCGCCATAAATGTGTTACCACTT
TGATTAGGGTCAAATGTAGTCTTTTCTAACTTGAAATTACTTGCCGTAACTTTATCATTT
ACATTTGTACCTTTAGCATCAGCAGCATTTACTACCGGTTCAGCAACAGCTAAACTACGT
ACAGCTCTCGTTCTAACACTTGGTTTACTAGTTCCTTGCGCATTGGAAATCGTTTGTGGT
GATGATTGTGGTAAATCTAATGTTTGAGAATTTTTAAGCTCACTGTTTGTTGCTATGCTA
TTAGCATCATTCGTTGTTTTATTATCTACTTGAGAATTTGCTTCTTGAGGAACAGTTTGA
TC
LOCUS 99 GE3
TTAATGATTTCTAACAATCTTAATGTTGCTACGACGTTTATTTCTTGAGATAAGATAGGT
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TCGTCAGCCAAACTTTTAATATTTTCTCGTTTACCTGTTCTATAGTTATCTAGAACATAA
ACATCATAATCTTGTTGTAAATCATCTACTAAATGCGACCCAATAAAACCAGCCCCACCA
GTTATCAAAACTCTTTCCAAATCTTCCACCTCATTTATACATTAAAAATATATCATAAAA
ACATAAAGTATTGTAAGCTTTTTATCGATATTTTTTATTTATAAAAATAAAATGAGATAA
CTTTGTGAATTTTTATTGAGATAAATTAGATAGTGGTGTTTTTGTGATGTTTTATAATAT
CTTGGGTGTGTTAATACTAATAATGCTTTCAACTGATGCATTAGACTGTGACATCATAAC
TCACTTAAGAACTTCGCTTATTAATTTTCTACCAATACACTCCCTTCTAAGTGCACTAAA
AAATCCTTACTGCTAAGTGATTAAACTTAACAATAAGGATTTATTTATCATTAGTGGATG
ATTATTAACGGAATCTCATACCACCATCTACAATAATTGTTTGTCCAGTAATGTAATCAG
AGTCTTTACCAGCTAAGAAGCTCACTACATTTGAAACATCTTCTGGTTGAGAAACTCTGC

CCAAAGCAATCTGACTTGTAAATTGTTCCCAACCCCATGCTTCAGGTTTACCTGCTTCTT
CGGCTGTTGCCACTGCGATACTTTCCATCATTGGTGTTTGAACGATACCAGGTGCGAATG
CATTCACAGTAATACCTTCAGACGCTAAATCTTGTGCGGCTACTTGTGTTAAACCTCGCA
CTGCGAATTTTGTACTGCAATATAAAGACAAGCCTGGGTTACCCTCAACGCCTGCTTGAG
ATGTTGCATTGATAATTTTACCGCCATGATTGAATTTTTTAAATTGTTCATGTGCGGCTT
GAATACCCCATAGCACACCTGCAACGTTCACGCCATATACTGTTTTAAACTGTTCTTCAG
TAATTGTATCGATTGGTGTTGTTGGTCCAAGGCCGGCATTGTTAACCATGACATGGAAAT
CGCCAAATTGCGCGGCAGTTTGTCTTACTGCGTTAAATACATCATCACGGTTTGATACAT
CTGCTTTGATAGCAATAGCTTTTGTACCATCACTTGATAATTTAAGTGCAGCTGCTTTTG
CCCCTTCTTCATTGAAATCAACAACTGCTACTTTGAAACCATCTTCCACTAAACGTTCTG
CAATTTTAAAACCAATCCCTTGTGCTCCGCCAGTTACTAATGCTACTTTGTTGTTTGTCA
TAAAGATC

LOCUS 100 GF5

GATCTACTTCTACAACTTTAGGCATGTCTGCTAAGTGAACACTTTCTTCTTTAACATGTG
GTGTATGAGACCAAACTTCTTCAGCTGTATGCACTAAGATTGGTGCTAACAACTTCGTCA
TATCAACTAAAATTTGATATAACACTGTTTGCATACTACGACGGATATGAGAATCACGTT
GTTCAATATATAAAATATCTTTACCGTAATCCAAATAGAAATTACTTAACTCAACATTGA
TAAAGTTTTGAACTTCTTGATAAATATTTAAGTAGTCAAAGTTTTCATAGTTGTTAATCG
TACTTGCAGTAAATTCACGTAAACGATTTAGCAAGTAACGATCCACTTCTAATAACTCTG
ATTCAGGAATGCTATCTGTGTCAGGATTGAAATCGTTAATGTTACCTAACATAAATCTTA
ATGTATTTCTGATTTTACGATAAACATCAGATGTTTGTTTTAAAATTTCATCAGAAATTC
TAACATCAGCTAAATAGTCCGTACTACTTACCCAAAGTCTCGCAATATCAGCACCTTTTT
GTTTAACCACTTGGTCAGGTACAATCACATTACCTAAAGATTTACTCATTTTCTTACCTT
CACCGTCCATAACAAAACCATGAGAAAGTAAGAATTTATAAGGTGATACTCCTCTTGTAG
CAACTGAAGTTGTGATAGAAGAGTTGAACCAACCACGATATTGGTCACTACCTTCTAAAT
ACATATCCGCTGGGAAACTTAATTCCGGTCTTGTTTCCAACACGCCACGGTGTGATGAAC
CAGAATCAAACCAAACGTCCATAATGTCTGTTTCTTTAGTAAATGTACCGTTAGGGCTGC
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AACCGTGTTCTGCAAATAAATCAGCAACATGATTCACTGTTTCTTTCGTCATGATAATTT
CGCCATTTTCAGCATAAAATACTGGTAACGGTACACCCCACACACGTTGACGAGAAATAA
CCCATTCGCCACGGTCACGAACCATATTGTAAATACGTGTTTTACCCCAATTTACTTTGA
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ATTGTGGTGTAGCACGGAAGATTACAGGTTTTTTTGTTCTCCAGTCGTGTGGATAGCTAT
GTGTAATAAAGTCTAATTTTAATAGTGCACCTTTTTCTGTTAATAAATCAGTAACGGCTT
TATTAGCTTTATCATAGAACATCCCTTCAAATTGGCCGCCTTCTTCAGTAAATACACCTT
TATCATCGATTGGACTAATTACTGGCAATTCATATTTTTGACCAACAATATAGTCATCTT
CCCCGTGACCTGGTGCTGTATGTACACAACCTGTACCAGCATCTGTAGTAACATGATCAC
CATTAATCACTAACGATTCTCTGTCTAAGAATGGATGTTGTGCTACAACATACTCTAATT
CTTTACCTGTGTATTCTTTTTCTAATTTGATTGATGCTTTATCCCAATCCAGTGCTTCTG
CTACAGCGTCAGACAAGGCTTCTGCAATAATATATTTTTCGCCATTTACATTGTATTGAC
CATATTTTAATTCAGGATGAACGGTAATCGCAACATTTGATGGAATTGTCCATGGCGTTG
TTGTCCAGATAATAAATTTAGCATCTGCATCAACGACACCTTTGTCATCTTTAACGTCAA
ATGCAACGTAAATTGATGCTGAACGTTTATCGTGATATTCAATTTCTGCTTCTGCTAATG
AAGACTCACTTGAAGGAGACCAATAAACTGGCTTTTTACCTTTATAAATTAAACCTTTAT
CTGCCATTTCTCCAAAAATACGAATTTGTGCAGCTTCGTATTCAGGTTTTAATGTAATAT
ATGGATC

LOCUS 101 (GF7)

GATCAAGTTCAAGGTTCATTAGAAATTATTTATAGTTTGCAAGAAGAATTAAAAGAAATT
ACTGGTATGGATGAGGTGACATTACAACCAGCTGCTGGCGCACATGGTGAATGGACTGCA

TTGATGATATTTAAAGCTTACCATGAGAATAATGGTGAAGGTCATCGTGATGAAGTCATT
GTGCCAGATTCTGCGCATGGTACGAATCCAGCCTCAGCTTCATTTGCAGGATTTAAATCA
GTTACTGTAAAATCAAACGAACGTGGCGAAGTTGATATTGATGACTTGAAACGTGTTGTA
AATGAAAATACAGCAGCTATTATGTTAACTAATCCAAACACTTTAGGTATTTTCGAAAAA
AATATTATGGAAATCCGTGAAATCGTCCATAATGCTGGTGGTCTATTATATTATGATGGT
GCGAATTTAAACGCTATTATGGACAAAGTTCGCCCAGGAGATATGGGATTTGATGCTGTT
CATTTAAACTTGCATAAAACATTTACTGGTCCACATGGTGGTGGCGGTCCTGGTTCAGGT
CCAGTCGGTGTAGTAAAAGAACTAGCAAGTTACTTACCAAAGCCAATGGTTATTAAAGAT
GGCGACAAATTTAAATATGATAATGACATTAAAAATTCTATCGGACGTGTAAAACCATTT
TATGGTAACTTTGGTATTTACTTAAGAGCTTATACGTATATTCGAACTATGGGAGCAACT
GGACTTAAAGAGGTTTCTGAAGCAGCGGTTCTTAATGCGAATTATATTAAAGCACGTTTA
TCTAAACACTTTGAAATACCTTATAAACAATATTGTAAACACGAGTTTGTGTTAAGTGGT
GTGCGTCAAAAAGAATTTGGTGTACGTACTTTAGACATGGCTAAGCGATTATTAGATTTC
GGTGTACATCCACCAACAATATACTTCCCATTAAATGTTGAAGAAGGTATGATGATTGAA
CCGACTGAGACAGAGTCTAAAGAAACACTTGATTATTTTATCGATACATTAATTAGTATT
GCTGAAGAAGCTAAAAATGATCCTGATAAAGTGCTAGAAGCACCACATACAACTGTGATT
GATCGATTAGACGAAGCTACAGCTGCTCGTAAACCAATATTAAAGTTTGAAAATCTTAAA
CAGGAAAAATAAAGTATTAAACACATATTCCGAGAATTATTATTCTAACTTTGTATGAAG
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CTAAACCGAAGTAATAACTCTTAGGGTTTGGTATTATTCTTTCATAGAAATTGTCTTTTC
ATTTTTTAGATTGCGGTAATTGAATCGTATTGAAAATGAGCTGAACTTTCTTTATTATGC
TGAAACTAAGTTTAATGATC
LOCUS 102 (GF9)
GATCCTGTGTTAACTGGTCGTTAAAAGTGACTTTCGTTTCAGTGTAAAATTTTTCTAATG
TAACAGATATGCTATTATTCATTGGAATGATTAGTGCTTCATCTTTTTTACCCCAATATT
TTATAAGTGCAATATTCGTATGTGCACGTGCTTTGCCACTTTTAATCAACGCATTAACCT
CCTAAATTCTCAATCCAAGTATGTGCTGCACCAGCTTTTTCTACAGCTTTTACAATATTT
TTCGCTGTTGGTAAATCTTTGGCAAGCAATAACATACTTCCACCACGACCAGCGCCAGTA
AGTTTTCCAGCAATCGCACCATTTTCTTTACCAATTTTCATTAATTGTTCTATTTTATCA
TGACTAACTGTCAACGCCTTTAAATCCGCATGACATTCATTAAAAATATCCGCTAAGGCT
TCAAAGTTATGATGTTCAATCACATCACTCGCACGTAAAACTAACTTACCGATATGTTTT
ACATGTGACATGTACTGAGGGTCCTCACAAAGTTTATGAACATCTTCTACTGCTTGTCTT
GTTGAACCTTTCACACCAGTATCTATAACAACCATATAGCCGTCTAAACTTAACGTTTTC
AACGTTTCAGCATGACCTTTTTGGAACCAAACTGGTTTGCCTGATACAATCGTTTGCGTA
TCAATACCACTTGGTTTACCATGTGCAATTTGCTCTGCCCAATTAGCCTTTTCAATGAGT
TCTTCTTTCGTTAATGATTTCCCTAAAAAATCATAACTTGCACGAACAAAAGCAACCGCG
ACAGCTGCACTCGATCCTAATCCACGTGATGGTGGTAAATTCGTTTGGATCGTTACTGCT
AGCGGCTCTGTAATATTATTTAATTCTACAAAACGGTTCACCAAAGACTTAAGATGGTCA
GGCGCATCATATAACATACCATCGTAAACATCGCTTTTAATAGACGAATAGTTCCCGCTC
TCTAAGGCTTCTATTAAAACTTTGATTTTACCTGCGTTAAACGGTACTGCAATAGCAGGC
TCTCCAAATGTAACAGCATGTTCTCCTATTAAAATAATCTTACCTGTCGATTCCCCATAT
CCTTTTCTTGTCATGTCAATATCACCTTTTATATTTATCCTATACTTGATTCATTATTTT
TATTTATTAGTAAAAGACATCATATTCTAAGTTGCATACGCATTCGCGTTAAATTTCATT
GCAGTCTTTATCTCACATTATTCATATTATGTATAATCTTTATTTTGAATTTATATTTGA
CTTAACTTGATTAGTATAAAACTAACTTTCGTTTACTTCAAAGTTTAAATCTTATCGAGT
GATATTTCAGATTCTTTATCTTTTTATAAAATAGCCCTACAATTTATAATTTTCCACCCT
AACTATAATACTACAAATAATAATTGGAATATATAGATTTACTACTAAAGTATTAGAACA
TTTCAATAGAAGGTCGTTTCTTTCATAGTCATACGCATTATATATACCCTATTCTCAATC
TATTTAATACGTAAAACATGAAATTTTCTTATTAAATTTATTATTTCCATCATATCATTA
CTTTTAATTTAATGATGTTCAATTTAAATATTAGGTCAATAACATATTTATGCTTTTTAT
GGATACTTTCAAAAATAACAGCCCCAAACGATAACTTGAAAGGGGCTGTTAAATATTTAA
CTATTGCATT

LOCUS 103 (GF11)

GATCATTCATTTTAAAGCCAGACTTTTTATAATCTTGTACAAATGCTTGCGCTACATCCT
TGTGTTGATCAAGCAATTCCCCTCTCAGTACTAGCACACAGCAATACGCATCAGGTATAA
CGTCATCACCATGTTTCAAAGTCTTACCTTTGCCTAACTTTTCACCCAGTGCACCGAATG
GTTCGGCTACAGAATACCCTGTAATTCTGTGTTCACTCAATGCGGCTGGCATTTCTGCTG
GCGACATTTCATGATAGCTAAAATGCCCCGGTTTAATCTTTAATTGTTTACGTAATTCCT
CAAGTAAAAGATAATGTGTTGAATAACGATGTGGTATACCAAAATGGTAATCATCGCCAT
TATTATTAAATTCATTTAAGTGCATACCTTTTTGTCCCATAATGACATTGCCTTCATGAT
GGCCCAATGCCACAGCCTTTATATTTGAGCCCTTCTGTTTTGATTTCATCGCTAGCTCTA
TTAAAGTTGATGCACCATCAATACGACCACTGTTTAATGCGTCCATTAAATCTGGCCAAT
TATTGAATTTAACTAATTCTAGTTTATATTTCGGATGATTGTATTGTGATAATAATTTTT
TAGTCATCATCAAATTAGCTGAATGTGTAATCGGCAAATATCCAATTTTAATCACTTGCT
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TAAAGATTCCAATGATGACGATTATGCTTAACCTTTTCATCGTCACTCACTCCTTATAAA
TAATATTCAGGTTCAACTTGATGATGATTCAATGCAAATGTTTCCATAATTTCATTACGA
ATCTTAAGTAGGTGGCTATCATTACGACTGCGTGGATGTGATGCTGTAATTTCATATTGA
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TCAATGTCATGCGTCACTAAAATAATAGTTGATTGCGTTTTATGTTTTAGTTGCACTAGT
TGATCCTGAAGTTTATAACGTGTAAATGCATCTAATGCACCTAATGGCTCATCCATCAAT
ATAACGTTAGGCTTATGCACATGCGCTCGACATAGTGCCACACGTTGTTTCATACCCCCG
GACAGTTGCTCGGGAAAATGCTTTCCCCTGTCTTCTAAATCAACTAATTTAAGCTGTGCG
TTAATCTCTTCATCACTAATTTTCTGTTGTAATCCAATCCTAATGTTGTCATTAATCGTT
TTCCATGGCAGCAAATTATGATGTTGAAATAGCATTAAACAATCTGGAGATGGCTGTTGT
TTAATTTCGTTATCAATAATGACACGACCAGACGATGGATGAATAAATCCACCGATAATA
TTGAGTAAAGTAGACTTTCCGCAACCACTTTTCCCTATGAAAGTGACTATTTCTCCCTTG
CTAATGTCCAAATTAAAGTTATGAATTACTTTATGTGATC

LOCUS 104 (GF12)

GATCGCCGATAAGTAAAAACGGTGCATTCATACGTTTCATCATATAATATCCTTCGAAAC
CTTCCGCTGTTCGATAACCACTAAAATATACGTTTAGTGGCGGTTTCATATCACCAGGGT
GGAAATAATAAATAAATTCCTGTCGTTGACTATCTACGAAACGACTACCACCAAGTAAAA
ATTGACCCATGTCTAATCTAGACCATCGTTTGTGTATAGGTCCTAAATGTACCGTCCCGT
TCCCACGCGCCTTAACAGTTACACTTATATAAGCATCAAATGGTTTCGCAGGTATCTCTA
AAGGACTGTCTAACATATCATCAGTCAATACGATTTGTTCAATTAATGCACCATCAGCGC
CAGTCTGAATCAATCTAAATGTATATTGCAACTCGACCGCACCATCAATATCAAATTCTG
GCCATATTTGAATGACTTTATCTTTATCGTAAACGAGATTATTTTGCCAAGATGCGATAG
GTTTAAATTCTTTCCCAAATTCTCCACTCAATGTGAGCTCTGAATTACCTTGGTAAACGA
CATCTCCTTTAAAATTCGGATGCACAAGTGCTAACTTAGGAGAAACCTTATCTCCATACT
GTCCTGAGAAGCTAACTGCCTCTAATTTATTATTACGTTCTTCAATATTCCGGTAATGTA
ATGGTTGAACAACGTATTTTTGGACATTTTCGTCTTGTTCATATTCAACTGACCAAAATG
ATTCATCAACATACGTATTGTATGGTTCGCTTATCATTTGTAATAAATTCGTTAATGTCT
CCGAGTATGGTGCTTGAATATAGATAAAATCAAAGCGCCCTTCTGCTTCAACAATCGCTT
CAATAGCCTCTACATAACCACTATCAAATTCAAACAATCCAATATCGAAGTAATCCCAAC
TCACACCTTTTTTGTGTTGAAAAATAGGTTCTAAATCGTCTCCTCCAATTTGCAAAACTC
TAAATTTACGTGGCATCATTTTCACCTTCTATTAACTCATCGAGCTGATTAATAATATTC
TTAGAAGCATATGCATCTATTAATTTTAAAGAATAGGCGTACGCATAATTCCAATTTTTC
AAATAAAATAAATAATAATTTAACGCATCATCTAATTCATCAACTGTATTTATAATACGG
CCATTGTCATAATCAGAGACGTAATCTGTTTGTTGACCATTAATTTGTGGAATCCCAGCG
CTAATTGCACTAATTTGTAAATACAAGTCAGGTTCTTTTGACATATCTATCACAAGTCGC
AACGTCCGCAATGCTTCTACAACATCATGTTCAGCATGTATCGTCTTAACAGCAATGATG
TCATCTTGATC

LOCUS 105 (E18)

ATCAAAAAGTTATGATGAACGTTTTACGCCGGATGAAGTAGTCGCATACCAACAACATCA
AGGTAATAAATTTAAAGAACATTTTGATTTGAATTGTTATCTGACACTGCTAGATGTATT
GGATAGTCACAACATTGACCGAGGTCGCACAGACGTAACGCATGTTTTTAAAAATTTAGA
AACAAAAGTGTTAACGATGGGGTTCATAGATGATTTGCTATATCCGGATGATC

LOCUS 106 (E101)

CTTCTAACATATTAACCCACTCGTTTGTAGCAGCGTTAAAACCAACACCCGGCTCTGCGT
TTTTCAAACGTTCTACAATAACAGAACCTTCTAATCCTGCATTTTCAGCAATTTGACGAA
CTGGTGCAGTTAATGCTTTAAGTACAATATTTACACCTGTTTCAATGTCACCTTCAGCTT
CAATTTCACTTACTTTTTGGTAAACATTTACTAATGCAGTACCACCACCTGCAACAATAC
CTTCTTCAACTGCTGCACGTGTAGAATTTAATGCATCTTCAATACGTAATTTACGTTCTT
TAAGCTCTGTTTCACTTGCTGCACCTACTTTGATAACTGCAACACCACCTGCTAATTTAG
CTAAGCGCTCTTGTAATTTTTCACGATC

LCOUS 107 (E110)

CGATATCTCCAAATTGTCTAATCAAGACCATTTGTACACCTTGCTTATCATTCTTTTTAT
CACTTAGCATATATTGGTATAACGTTTCAAAATCCAAGTCAGTTATCATGTCTAAAGGAT
AGCCGAGTTGTATTAAATATTGAATATAATGATTAATATCATGCTTAGAATCAAACAAAG
CATTCGCAACTATAAATTGATAGATAATGCCAACCATCACTGCATGACCATGAGGTATTT
TATGATAGTATTCAACAGCATGACCAAATGTATGACCTAAATTTAAAAATTTACGTACAC
CTTGTTCTTTTTCATCTGCAATAACAATATCCAGCTTCGTTTCAATACCTTTAGCAATAT
ATTTATCCATACCATTTAATGACTGTAATATCTCTCTATCTTTAAAGTGCTGTTCGATAT
CTTGCGTCGCTGATTCACCATTCAATAACGCATGCTTATAAACTTCTGCATAGCCACTTA
ATATTTGCTCAAATGGTAACGTCTTTAAAAAGACTAAATCATAAATCACAGCAGTTGGAC
GATAAAATGCACCGATAAGGTTTTTACCTTGCTTTGAGTTAATACCCACTTTACCGCCAA
CACTAGAATCATGCGCTAGTATAGTCGTTGGCACTTGTATAAAGTGCACGCCTCGTAAAA
GTGTCGCCGCAATAAACCCAGCAAAATCACCAGTTGCACCACCACCAACAGCAATAATTG
CTGTATTACGAGTTACATGATGGGATAAAATATACTCTAATGTTTCTTGATATTGCTCAA
ATGTTTTCGTCTTTTCACCAGCTGGAATAATAACTTTATGTACATTTTCATATGATAAAA
TATCATCAAATTTATCAGCAAAATATTGATTTACATGCTCGTCAATTAATATAAAACTTT
GATCAAACTGATCAATATACGTGCTAATATGGTCAATTGCACC

LOCUS 108 (E125)

CACTTTTGAATGTTCACTTCTAAAGATTTGGTCTGTAACTTCCATTTCAGCTAATCCATA
TTTTTCATAAATTTCTTGTCCATAAAGTGTATTTGTATCATGGAATGCTGGTAAACAATG
TAAGAATATCGTTGAATCTTTACCTGTTAAATCAAACATCTGTTGATTCACTTGATAGTC
TTTTAATAAATTAATACGTTGTTCAAATTCACTTTCTTCACCCATCGATACCCAAACATC
TGTATATATAGCATCTGTATTTTCAACTGCTTCTGCAATATTATCCGTAATCATGACTGA
ACCACCATATTGACTCGCTTTTTCTTTTGCAATATCAACATATGCCTCTTTTGGATTTAA
TGATTTAGGTGTACAAATTCTTACATTAACACCTAACATAGCACCTGCTACCATTAATGA
ATGCGCAATATTATTACGTCCATCTCCAACGTAAGTTAAGTTTATTCCTTCTAGATATCC
AAAATTCTCTTTTATTGTCATAAAATCAGCTAACATTTGTGTAGGATGCCAATCGTCTGT
TAATCCATTCCACACCGGTACACCAGAGAACTTCGCTAAATCTTCAACAGCTTGTTGTGA
AAAACCACGGAATTCAATACCATCGAACATTCTACCTAATACTTTCGCAGTATCCTCTAC
AGATTCTTTTTTGCCTAATTGAATATCATTTTTTCCTAAAAATTCTGGATGCGCACCTAA

ATCAATAGACGCAACTGTAAACGCAGCACGCGTTCTCGTCGAATTCTTTTCGAATAGTAG
TGCAATATTTTTTCCAGATAAGTAGTGATGCTTAATACCGTTTTTCTTATACTCTTTTAA
TGTAATTGCAAAATCAATAAGTCCTTCGAATTCTGCTTTGGTAAAATCACTTTCTTTTAA
TAATGATCTGCCTTTTAAATCATACGGTTTTTGAATTTCTGTCATTATTTTCACCCTCGT
TTCTATAATTTATTACGTTAAATGTCCTCTCTGAATAATGGTTGACTCATACATCTAGGG
CCCCCACGTCCACGTACCAACTCGCTACCAGATATTTCAATGACTTTAATGCCTTTTTGT
CTCAATAAATCATTCGATACATAGTTTCTATCGTAAGTCACTACAACGCCTGGTCTTATA
CATAATGTATTTGAGCCATCATTCCATTGCTCTCTAGCACCATCAATGACATCACCATTT
CCTGTTGGAATGAATTGGATATCATCTATACCTAGTACGTCTTCTAAAGTATCTTTTAAA
TGACTAGATTGTTTGATGGCAATATCTTTATTTACGTCATCATATTCAATAATAAATATA
TTCATATTGCCTTCTGCCTTTAAAATGGCTGAATGCATTGTAAATTTGTCATAATCTATC
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ACTTTTTTAAACGTCGCCTGCGGATTTTCAAAAATACGTCGCGCTAACTTTTCAATAGCT
TGTGCAGATGTACGTTCTGAAACGCCTATAGCCAAGACATCTTTAGATAAAACAAGTTCA
TCGCCGCCTTCAATATTGAATGGGCAATCTCGATC
LOCUS 109 (F101)
CAATACCTTGTGGACAAATAAGTATGACATCTTGATTATCTACATTAAAGTAATCTGGGC
ATTCCCACATATATCCAAAATCATCCAACTCTGTATTTATTTCACCTAAATAATGCCAAT
TAATTATATCTTCAGTATTATAAAGTAATAATCGACCTTGCTGATCATTATTTTGTGCAC
CAATGATTGCATAATATTTCTCATCATATTTAAAAACTTTAGGATCTCTAAAATGACTCG
TATATCCTTCTGGTTGTTGGCTAATTACTGGCTTTGGAAACTTTTCAACTGAACCGTCTT
CTTTCAATCGTGCGATCATCTGACTCGCATGTCGTTGCCAATGATTATCTCGATGATTTC
CTGTGTACATATAATATAAATGCCCGTTATATTCAAAAGCGCTACCGCTATATACACCAT
GGCTGTCATATTTAGTATCTGGATTTAAAATTGGCCCTTCAGCTTTAAAGTTTATTAAGT
CATCACTCGTGTAGTTATACCAATACTTTAAGCCATGTACTGCGCCTAATGGGAACCATT
GATGTGAAACATAATACTTCCCTTTATAAAAAATAAGTCCGTTGGGGTCATTTAATAAGC
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ATTCGGTCATAATATTTACCCAGTCCTCCTTTTATAATTTATGCTGTTAACAATTTATAT
TCTATTATAGCAAATTTTACCTACGTTCTTTAACTTTTAACCTATCCATTTATAGTTATA
TGGTATCGGTTCCACATTTATTTTAAAAAATACAGCGTCTAAATATTAACATCTACTGTG
ACGCTATATGGCATATCTTGCTTTTTAAGCATCTGTTGTATCTCTTCCATCGCGCATTGG
CCAGCTTCAAAATAATTATAATGAATTGTTTTTATCGATGGAGACACTAATTGTGTCATT
GGGTCACCACCAAAACCATATATTTGATGTGGTTTCATAACATCTTTTTTATCAGAATAA
TATTTATAGGCAGCTAATGCAATCGTATCAGTTGCTCCAACAACCGCATCTACTTGCTCC
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TGACCAATCCATTCGCCTATAATTTGACCTGCTTTATAATCATCATGCACAATACTATGA
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AATGTTTCAAGCGCTTGTATTTCTGCTTCGATATTTAAACCTGTGTAATTTAAAATTAAT
TGTGATTCATATTTTTGGCATTGTTTTGCCAATCCTTTGATTGTTTCATCTACTGCATAT
GAATTCATTCTAGGTATAATGGCACCAATAAGGTGTGTTTGTCTCGCTCTTAAACTTTGA
GCAAATTGATTCGGTTGATAGTCATGTTCTGCTATAATTCTTGTTAATTTTTCACTTGTT
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AATTTGGCAATATCAGATATATTTTTCATACTTATTCACCTATCATTATTTGTGACACTT
AGCCTTATTTTAGCATATGTGTAACCGCTTTAAATAATATTTCTGCTTCTTTCATAAAAA
GATTTCAAAATAAAACTTTTGTATAACAAAATGTCCCAACATCAACCTTTAGTTAAATGT
CAGGACAATGAATATTCTATGTAAATATATTCTAATATCGAATATGTTTATTGAATCTAT
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TTTCTTGTTCCGTAACAGATAATGGTGTAATTAATTTAATTACTTTCGCAATAATAAACG
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GTATGTCACCAGTATAAATAAAGCCATTCTCAATGTCAGGATTGGCTTTTTTACTTTGGA
AAACTGCTGTTAAAACAGCACCAATAATACCACCAACACCATGAATACCAAATGCATCTA
ATGCATCATGATATTTTAGTTTTACCTTGATGTAATTAATGACAATATAACAACAGATAC
CTCCTATTAAAGCCATTATTGTTGCACTAAGATATGTTACATATCCTGCTGCAGGAGTAA
TGACAACTAATCCTGCTAATGCACCGAGTAAAAGTCCAAGTAAACTTGTCGTCTTTTTAA
AAATATATTCTAAAATTAACCAACCTATAGCACCTGCACTGGCTGAAATGACAGTATTTG
TAAATGCAAGCATCGCAATATTATCAAATGTAAAAGCACTACCTACATTAAATCCATACC
AACCAATCCACACGAATATACCGCCAATCAACGTAATGATAAGATTATGTGGTGTTGATT
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LOCUS 110
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LOCUS 111
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LOCUS 112

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LOCUS 113
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LOCUS 115
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TABLE 8

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LOCUS 6 (D1)
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LOCUS 7 (D1)
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LOCUS 8 (D4)
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LOCUS 9A (D22) AA SEQUENCE
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LOCUS 9B (I2) AA SEQUENCE
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LOCUS 12 ()
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LOCUS 17 (I3)
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PGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFLTKFADKVTIVHRRDELR
AQRILQDRAFKNDKIDFIWSHTLKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGM
KPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSA
AEYIEHLND
>G2387_STAAU8325, UNDEFINED PRODUCT 2275222:2276658 REVERSE MW:57062
HYRLYGIFLLDQLNGKEIVM
TESIWQVLENLNNYEKLYLTYLVQGLTLNKLDFIHRGLLTLYHNELFVSENDVMVAWINQ
GELIIAEKVDLTDVEPYIGAFIYLYFKNQPRNVTKKQITTWLGITQYKLNKMIEFLLSI
LOCUS 19 (I8)
>G2296_STAAU8325, UNDEFINED PRODUCT 2195143:2196150 REVERSE MW:37749
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LAKQLSELDLASHPFVMSEQFASLKDRPFHPLAKEKRGLREADYQVYQAELNQSFPLMVA
AVKKTHMIHGDTANIDELENLTVPIKEQATDMLNDQGLSIDDYVLFPVHPWQYQHILPNV
FAKEISEKLVVLLPLKFGDYLSSSSMRSLIDIGAPYNHVKVPFAMQSLGALRLTPTRYMK
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AKNDTQQLVSMAALAANDRTLYQMICGKDNISKNDVMTLFEDIAQVFLKVTLSFMQYGAL

PELHGQNILLSFEDGRVQKCVLRDHDTVRIYKPWLTAHQLSLPKYVVREDTPNTLINEDL
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>G2294_STAAU8325, UNDEFINED PRODUCT 2192119:2193372 REVERSE MW:44835
MINQSIWRSNFRILWLSQFIAIAGLTVLVPLLPIYMASLQNLSVVEIQLWSGIAIAAPAV
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ASSAFASAEAPAEDRGKVLGRLQSSVSAGSLVGPLIGGVTASILGFSALLMSIAVITFIV
CIFGALKLIETTHMPKSQTPNINKGIRRSFQCLLCTQQTCRFIIVGVLANFAMYGMLTAL
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LOCUS 20 (J7/M10)
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>G2186_STAAU8325, UNDEFINED PRODUCT 2067945:2068697 REVERSE MW:28498
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FEELQKHTDLILLDIKHIDNDKHIRLTGKPNTHILNFARKLSDMKQPVWIRHVLVPGYSD
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>G2185_STAAU8325, UNDEFINED PRODUCT 2065846:2067657 REVERSE MW:69718
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IGHRGFEDKGVENSIPSLKAAAKANVEYVELDTIMTKDKQFVVSHDNNLKRLTGVNKNIS
ESNFKDIVGLKMRQNGHEAKFVSLDEFIETAKQSNVKLLVELKPHGKEPADYTQRVIDIL
KKHGVEHQYRVMSLDYDVMTKLKKEAPYLKCGYIIPLQFGHFKETSLDFFVIEDFSYSPR
LVNQAHLENKEVYTWTINGEEDLTKYLQTNVDGIITDDPALADQIKEEKKDETYFDRSIR
ILFE
>G2184_STAAU8325, UNDEFINED PRODUCT 2065335:2065676 FORWARD MW:12828
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>G2183_STAAU8325, UNDEFINED PRODUCT 2063238:2065145 REVERSE MW:71718

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NPRTDLKMANFHKYNLEELSMKEYNELQDALKRALDDFHREVKDIKDKNSDLKTFNAAEE
DKATKEVYDLVSEIDTLVVSYYGDKDYGEHAKELRAKLDLILGDTDNPHKITNERIKKEM
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EGSSSKLEIKPQGTESTLKGTQGESSDIEVKPQATETTEASQYGPRPQFNKTPKYVKYRD
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>G2181_STAAU8325, UNDEFINED PRODUCT 2061438:2062628 FORWARD MW:42182
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GVELMSAVPMGGNEPTNNPTLQYDDIGASYPMGLTAENVASQFDVSREDQDAYAVRSHQR
AYDAQRDGRFKDEIIPIQVNSVEYTNAGPKVHTNIFDQDEFIRPDTTMEALAKLRTVFKA
DGTMTAGTSAPLSDGAGFVVLMSGDKVKELGVTPIARFVGFKAVGVDPKIMGIGPAYAIP
EVLSLSNLSVEDIDLIELNEAFASQTIASIKEVGLDISRTNVNGGAIALGHPLGATGAML
TARLLNEMGRRPDSRYGMVTMCIGVGMGAAAIFEYVR
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FDLNLASHLTYGNFDDDLVNDDADLYIEAVKEDIEIKHAVWQQVLQHAKEDALFATNTSG
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VIVVNDVPGFVANRVGTQTMNDIMYRAEQHKISIVDVDALTGQAIGRPKTGTYALSDLVG
LDIAVSVIKGMQQVPEETPYFHDVKIVNTLFDNGALGRKTKQGFYKKDKETKARLVYDVE
KQDYVPVSQPQLPILNEFNKDLVHNLDTIFNAQDEAGLFLWETLRNNFYYSAINVPKATD
DFRDIDRALVWGFNWKLGPFQLWDAMGYERVKTRMEDELGDLPQWISDLDGGFYKQDETI
EYATPISHFVKDELWDKGDAKLSVTHDDQLLLKLQSKNNVITDEFNDALVDAIDLLENDH
YTSMVIYADGNNFSVGANLFLMKKAHEDGLVDDVVAQSIDKLHYSFNRLKYSLKPVVTAV
QGRALGGGCELVLYSPIVVAASETYIGLVEAGVGLLPSGGGLAEMADRILRTSHKFDDKQ
ASMTKVLTNIAFAKVSTNAFEARRYGYLRDTDTIIFNTAQRVEVALKRAKYEAETNYIPN
PRHQYIALGEDFKALIQGQLDAQRRGHFISDHDYHIALNIATILAGGDLPRNTFINQRYI
QSLEKIGFIDLLKSKKSYERIAHMLKTGKPLRN
>G2179_STAAU8325, UNDEFINED PRODUCT 2057714:2058967 FORWARD MW:46482
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NINQHWIDATVPEDYFKDLGELNYFNNPLLYKDRPNAKMPSQLFQFFMSYLLARFDISLA
TLLGVHQGLGHNTFYFGGSKEQIAKYVPKLQSHELRTCFALTEPEHGSDVAGGLETVAER
QGDTWVINGEKKWIGGAHVSDVIPVFAVNKETGKPHCFVVRPEQDGVDIEVIDNKIALRI
VPNALIKLTNVKVDEADRLQNITSFKDIAKILYSTRAGVAYMATGGMAGALRATLDYVTE
RKQFGKPISKYQLIQEKLAMMQGNLAQAMATCAQLANMQAHGEYDEVATSTAKMMNALRL
RETVAMGRGITGGNGILADDYDIARFFSDAEAIYTYEGTHEINALVIGRALTGDSAFV

LOCUS 21 (G3)
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>G1928_STAAU8325, UNDEFINED PRODUCT 1810990:1811910 REVERSE MW:32866
MANLQKYIEYSREVQQARENNQPIVALESTIISHGMPYPQNVEMATTVEQIIRNNGAIPA
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VIGYQTNELPAFFTRESGVKLTSSVETPERLADIHLTKQQLNLEGGIVVANPIPYEHALS
KAYIEAIINEAVVEAENQGIKGKDATPFLLGKIVEKTNGKSLAANIKLVENNAALGAKIA
VAVNKLL
G1929
LDHVQQFENASTGSYTALISKEGDMTYGLADMEVFDYITPE
FLIKRSHLLKKAKCIIVDLNLGKEALNFLCAYTTKHQIKLVITTVSSPKMKNMPDSLHAI
DWIITNKDETETYLNLKIESTDDLKIAAKRWNDLGVKNVIVTNGVKELIYRSGEEEIIKS
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LYHDMEDYKNGKFTKVY
LOCUS 22 (I19)
>G0974 FRG_STAAU8325, UNDEFINED PRODUCT 974673:975977 REVERSE MW:47346
VNEMVNEQIIDISGPLKGEIEVPGDKSMTHRAIMLASLAEGVSTIYKPLLGEDCRRTMDI
FRLLGVEIKEDDEKLVVTSPGYQSFNTPHQVLYTGNSGTTTRLLAGLLSGLGIESVLSGD
VSIGKRPMD
>G0975_STAAU8325, UNDEFINED PRODUCT 975981:977042 REVERSE MW:40300
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KVIIPAGEKTKTFEQYQETLEYILSHHVTRNTAIIAVGGGATGDFAGFIAATLLRGVHFI
QVPTTILAHDSSVGGKVGINSKQGKNLIGAFYRPTAVIYDLVFLKTLPFEQILSGYAEVY
KHALLNGESATQDIEQHFKDREILQSLNGMDKYIAKGIETKLDIVIADEKEQGVRKFLNL
GHTFGHAVEYYHKIPHGHAVMVGIIYQFIVANALFDSKHDINHYIQYLIQLGYPLDMITD
LDFETLYQYMLSDKKNDKQGVQMVLIRQFGDIVVQHVDQLTLQHACEQLKTYFK
>G0976 FRG_STAAU8325, UNDEFINED PRODUCT 977071:978240 REVERSE MW:43249
DFYDSETFKANLDRNDVRVIDDSIAQAMRDKIDEAKNEGDSIGGVVQVVVENMPVGVGSYVH YDRK
LDGKIAQGVVSINAFKGVSFGEGFKAAEKPGSEIQDEILYNSEIGYYRGSNHLGGLEGGMSN GMPIIVNGVMKPIPTLYKPLNSVDINTKEDFKATIERSDSCAVPAASIVCEHVVAFEIAKAL LEEFQSNHIEQLKQQIIERRQLNIEF
LOCUS 24:
G0243FRG
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>G0244_STAAU8325, UNDEFINED PRODUCT 218549:220261 FORWARD MW:61780
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RVTRDDVNVADLVISNAVIIDYDKVVKADIGIKNGYIFAIGNAGNPDIMDNVDIIIGSTT
DIIAAEGKIVTAGGIDTHVHFINPEQAEVALESGITTHIGGGTGASEGSKATTVTPGPWH
IHRMLEAAEGLPINVGFTGKGQATNPTALIEQINAGAIGLKVHEDWGATPSALSHALDVA
DEFDVQIALHADTLNEAGFMEDTMAAVKDRVLHMYHTEGAGGGHAPDLIKSAAFSNILPS
STNPTLPYTHNTVDEHLDMVMITHHLNAAIPEDIAFADSRIRKETIAAEDVLQDMGVFSM
ISSDSQAMGRVGEVITRTWQVAHRMKEQRGPLDGDFEHNDNNRIKRYIAKYTINPAITHG
ISEYVGSIEPG
>LOCUS 25:
G0027_STAAU8325, UNDEFINED PRODUCT 32103:32513 REVERSE MW:16524
MNEYRNKKGPDYSIFKNNWKVLLMDTSKTIFSKYRWNKSFKAYKRSSDIVEFMLSKDDIL
RHSYELVQGLRKDLRLCNWPKFINRLNSVSKKSVSKGVWKVVKYYRKHQRMLRNTIYYPA
FNNGAIEGINNKIKLIK
LOCUS 26:
>G2458FRG_STAAU8325, UNDEFINED PRODUCT 2348221:2350185 REVERSE MW:69055
VKIMRVTELLTKDTIAMDLMANDKNGVIDELVNQLDKAGKLSDVASFKEAIHNRESQSTT
GIGEGIAIPHAKVAAVKSPAIAFGKSKAGVDYQSLDMQPAHLFFMIAAPEGGAQTHLDAL
AKLSGILMDENVREKLLHASSPEEVLAI
>G2459_STAAU8325, UNDEFINED PRODUCT 2350185:2351102 REVERSE MW:32573
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GFPGKFIIDTLNNSAIQSNFIEVDEDTRINVKLKTGQETEINAPGPHITSTQFEQLLQQI
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NKDELEVMFNTTVNSDTDVIKYGRLLVDKGAQSVIVSLGGDGAIYIDKEISIKAVNPQGK
VVNTVGSGDSTVAGMVAGIASGLTIEKAFQQAVACGTATAFDEDLATRDAIEKIKSQVTI
SVLDGE
G2460FRG
DRTGCSASTIRRDLSKLQQLGKLQRVHGGAM
LKENRMVEANLTEKLATNLDEKKMIAKIAANQINDNECLFIDAGSSTLELIKYIQAKDII
VVTNGLTHVEALLKKGIKTIMLGGQVKENTLATIGSSAMEILRRYCFDKAFIGMNGLDIE
LGLTTPDEQEALVKQTAMSLANQSFVLIDHSKFNKVYFARVPLLESTTIITSEKALNQES
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LOCUS 27:
G1326FRG
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>G1327_STAAU8325, UNDEFINED PRODUCT 1284689:1285450 FORWARD

MW:27870
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NIFPYTGVVAFKSATGFVVGKNTILTNKHVSKNYKVGDRITAHPNSDKGNGGIYSIKKII
NYPGKEDVSVIQVEERAIERGPKGFNFNDNVTPFKYAAGAKAGERIKVIGYPHPYKNKYV
LYESTGPVMSVEGSSIVYSAHTESGNSGSPVLNSNNELVGIHFASDVKNDDNRNAYGVYF
TPEIKKFIAENIDK
>G1329_STAAU8325, UNDEFINED PRODUCT 1285505:1286227 FORWARD MW:26340
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Q
>G1330_STAAU8325, UNDEFINED PRODUCT 1286327:1287067 FORWARD MW:26652
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GVTWMGAGTGFVVGNHTIITNKHVTYHMKVGDEIKAHPNGFYNNGGGLYKVTKIVDYPGK
EDIAVVQVEEKSTQPKGRKFKDFTSKFNIASEAKENEPISVIGYPNPNGNKLQMYESTGK
VLSVNGNIVTSDAVVQPGSSGSPILNSKREAIGVMYASDKPTGESTRSFAVYFSPEIKKF
IADNLDK
>G1332_STAAU8325, UNDEFINED PRODUCT 1287228:1287941 FORWARD MW:25679
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TGFIVGKNTIVTNKHVVAGMEIGAHIIAHPNGEYNNGGFYKVKKIVRYSGQEDIAILHVE
DKAVHPKNRNFKDYTGILKIASEAKENERISIVGYPEPYINKFQMYESTGKVLSVKGNMI
ITDAFVEPGNSGSAVFNSKYEVVGVHFGGNGPGNKSTKGYGVYFSPEIKKFIADNTDK
>G1333_STAAU8325, UNDEFINED PRODUCT 1288095:1288811 FORWARD MW:25655
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EEKSTQPKGRKFKDFTSKFNIASEAKENEPISVIGYPNPNGNKLQMYESTGKVLSVNGNI
VSSDAIIQPGSSGSPILNSKHEAIGVIYAGNKPSGESTRGFAVYFSPEIKKFIADNLDK
>G1334FRAG._STAAU8325, UNDEFINED PRODUCT 1288994:1290730 FORWARD MW:66904
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SGEDITYQEAWADEEYREDLKAELID
ORF1 (AF7)
SGTGFIVGKNTIVTNKHVVAGMEIGAHIIAHPNGEYNNGGFYKVKKIVRYSGQEDIAILH
VEDKAVHPKNRNFKDYTGILKIASEAKENERISIVGYPEPYINKFQMYESTGKVLSVKGN
MIITDAFVEPGNSGSAVFNSKYEVVGVHFGGNGPGNKSTKGYGVYFSPEIKKFIADNTDK
ORF2 (AF7)
MNKNIIIKSIAALTILTSITGVGTTMVEGIQQTAKAENTVKQITNTNVAPYS
GVTWMGAGTGFVVGNHTIITNKHVTYHMKVGDEIKAHPNGFYNNGGGLYKVTKIVDYPGK
EDIAVVQVEEKSTQPKGRKFKDFTSKFNIASEAKENEPISVIGYPNPNGNKLQMYESTGK
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IADNLDK
LOCUS 28 (H130)
>G1388_STAAU8325, UNDEFINED PRODUCT 1337496:1338446 REVERSE MW:36053
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GDFAGNRADSIAVQFKEIKEKMHEKWHEGKYIAYFQAFTNTHAPVEVLKEKFEPVLKEPG
VVGLSIGTRPDCLPDDVVEYLADLNQRTYLWVELGLQTIHQSTSDLINRAHDMKTYYDGV
AKLRKHNINVCTHIINGLPGEDYDMMMATAKEVAQMDVQGIKIHLLHLLKGTPMVKQYDK
GLLTFMTQEEYTNLVVDQLEVIPPEMIVHRITGDGPIDIMVGPMWSVNKWEVLNGIDAEL
ARRNSYQGLRYKSKVKQ
>G1389_STAAU8325, UNDEFINED PRODUCT 1338556:1339734 FORWARD MW:43345
MNIPKSVWWLVIGMALNITGSSFLWPLNTIYMKQELGKSLTVAGLVLMINSFGMVIGNLL
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AVWPNGGRQTFNAIYLAQNIGVAVGAAMGGFVAEFSFNYIFLANLIMYVVFALVAVTQFN
IEINAKVKYPTHLDITGKKNKARFISLVLICAMFAICWVAYIQWESTIASFTQSINISMA
QYSVLWTINGIMILVAQPLIKPILYLLKGNLKKQMFVGIIIFMLSFFVTSFAENFTIFVV
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>G1390_STAAU8325, UNDEFINED PRODUCT 1340025:1342439 FORWARD MW:91754
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KSGVFTGAYATNPLSGEKVQIWIADYVLSTYGTGAIMAVPAHDDRDYEFAKKFDLPIIEV
IEGGNVEEAAYTGEGKHINSGELDGLENEAAITKAIQLLEQKGAGEKKVNYKLRDWLFSR
QRYWGEPIPVIHWEDGTMTTVPEEELPLLLPETDEIKPSGTGESPLANIDSFVNVVDEKT
GMKGRRETNTMPQWAGSCWYYLRYIDPKNENMLADPEKLKHWLPVDLYIGGVEHAVLHLL
YARFWHKVLYDLAIVPTKEPFQKLFNQGMILGEGNEKMSKSKGNVINPDDIVQSHGADTL
RLYEMFMGPLDAAIAWSEKGLDGSRRFLDRVWRLMVNEDGTLSSKIVTTNNKSLDKVYNQ
TVKKVTEDFETLGFNTAISQLMVFINECYKVDEVYKPYIEGFVKMLAPIAPHIGEELWSK
LGHEESITYQPWPTYDEALLVDDEVEIVVQVNGKLRAKIKIAKDTSKEEMQEIALSNDNV
KASIEGKDIMKVIAVPQKLVNIVAK
LOCUS 29A (N10/GE2)
>G2804_STAAU8325, UNDEFINED PRODUCT 2682166:2682924 REVERSE MW:29096
MAYISLNYHSPTIGMHQNLTVILPEDQSFFNSDTTVKPLKTLMLLHGLSSDETTYMRYTS
IERYANEHKLAVIMPNVDHSAYANMAYGHSYYDYILEVYDYVHQIFPLSKKRDDNFIAGH
SMGGYGTIKFALTQGDKFAKAVPLSAVFEAQNLMDLEWNDFSKEAIIGNLSSVKGTEHDP
YYLLDKAVAEDKQIPKLLIMCGKQDFLYQDNLDFIDYLSRINVPYQFEDGPGDHDYAYWD
QAIKRAITWMVND

>G2805_STAAU8325, UNDEFINED PRODUCT 2683043:2685673 REVERSE MW:93576
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ADSEKNNMIETPQLNTTANDTSDISANTNSANVDSTTKPMSTQTSNTTTTEPASTNETPQ
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LOCUS 45
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RKFNPDLAPGTEKVTREGQKGEKTITTPTLKNPLTGEIISKGESKEEITKDPINELTEYG
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KGDSIVEKEEIPFEKERKFNPDLAPGTEKVTREGQKGEKTITTPTLKNPLTGEIISKGES
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DVIKHGPKTGTPETKTVEIPFETKREFNPKLQPGEERVKQEGQPGSKTITTPITVNPLTG
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LOCUS 47 HF6
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>G2561_STAAU8325, UNDEFINED PRODUCT 2441159:2444143 REVERSE MW:107795
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LOCUS 49 K16
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>G1542_STAAU8325, UNDEFINED PRODUCT 1495403:1497337 FORWARD MW:72192
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G1544
>G1544_STAAU8325, UNDEFINED PRODUCT 1497751:1497846 REVERSE MW:3849
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G1456
>NONE, UNDEFINED PRODUCT 1497815:1498165 REVERSE MW:12767
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LOCUS 50 GB2
>G1392_STAAU8325, UNDEFINED PRODUCT 1343118:1349675 FORWARD MW:238192
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QQHIAEINANPDATQEERQAAIDKVNAAVTAANTNILNANTNADVEQVKTNAIQGIQAIT
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EVAQAKDQGTQNIVVIQPATQVKTDTRNVVNDKAREAITNINATTGATREEKQEAINRVN
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LAQINQHYNAKLAEINATPDATNDEKNAAINTLNQDRQQAIESIKQANTNAEVDQAATVA
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LOCUS 50 G10

>G1392_STAAU8325, UNDEFINED PRODUCT 1343118:1349675 FORWARD MW:238192
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ENNID
LOCUS 51 (GC8)
>G2831 FRG_STAAU8325, UNDEFINED PRODUCT 2720353:2721114 FORWARD MW:27865
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NLRGFSALDSGLLLLPGSLIMGLLGPFAGKLLDTIGLKPLAIFGIAVMTYATWELTKLNM
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VTVMTTQTTQHLSAFGEELDKTNP
>G0407 FRG_STAAU8325, UNDEFINED PRODUCT 372110:372754 REVERSE MW:23024
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>G2245_STAAU8325, UNDEFINED PRODUCT 2143358:2144242 REVERSE MW:33683
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>G2246_STAAU8325, UNDEFINED PRODUCT 2144245:2144799 REVERSE MW:21063
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>G2255_STAAU8325, UNDEFINED PRODUCT 2153408:2155321 REVERSE MW:72361
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IIAIPTIGQERLKEINNICHMDGVELLKMPNIEDVMSGELEVNQLKKVEVEDLLGRDPVE
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>G2256_STAAU8325, UNDEFINED PRODUCT 2155251:2156012 REVERSE MW:29362
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MPQQDYKQKRWFGL
LOCUS 55 (E18)
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LOCUS 56 (F5)
>G1261 FRG_STAAU8325, UNDEFINED PRODUCT 1216923:1217903 FORWARD MW:36061
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>G1262_STAAU8325, UNDEFINED PRODUCT 1217919:1219190 FORWARD MW:46726
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SFKNKEGYNLTFFAFFVKAVADALKAYPLLNSSWQGNEIVLHKDINISIAVADENKLYVP
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AAILQVESIVKKPVVINDMIAIRNMVNLCISIDHRILDGLQTGKFMNHIKQRIEQYTLEN TNIY
>G1263_STAAU8325, UNDEFINED PRODUCT 1219532:1219978 FORWARD MW:16676
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GIARPAASHALHYDVLPDRLVTVFAGQDKEATQRAREYFEGYAPSSPSFALVKDGKITEM
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>G1264_STAAU8325, UNDEFINED PRODUCT 1219995:1220972 FORWARD MW:36973
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LVSCFLVLFLGSAIFSLLGQSPIVLGIIVLLFIPLTVVLKVQEGVITSCVILLHVFNAKS
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LOCUS 57 (F3)

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>G0452_STAAU8325, UNDEFINED PRODUCT 412872:414536 FORWARD MW:60909
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ILIQSSSGTTVITIGLVTAGFMTLKQAIGVIMGANIGTTVTAFIIGIDLGEYAMPILALG
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LOCUS 58 (G8)
>G0922 FRG_STAAU8325, UNDEFINED PRODUCT 915062:915931 REVERSE MW:33411
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LOCUS 59 (G23)
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>G2455_STAAU8325, UNDEFINED PRODUCT 2345162:2346508 REVERSE MW:51133
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LOCUS 60 (G29)
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>NONE, UNDEFINED PRODUCT 137582:139645 REVERSE MW:75349
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DGDLMEGISHEAASFAGHNKLSKLVVLYDSNDISLDGELNKAFSENTKARFEAYGWNYLL
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FIFTHDSIAVGEDGPTHEPIEQLAGLRAIPNMNVIRPADGNETRVAWEVALESESTPTSL
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LOCUS 61 (G28/HA7)
>G2610_FRG STAAU8325, UNDEFINED PRODUCT 2494989:2495441 FORWARD MW:17293
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>G2611_STAAU8325, UNDEFINED PRODUCT 2495615:2497207 REVERSE MW:58937
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SEKMGPELRQYLFSGDNEGKPFSRNDYKNIVLAGKYNSRMTSFGTTKDYQDGFYIQNTMF
PMQRNEISVDNTTLLSTFIYKIANERLFSREEYRVPTKIDPYYLSDDHAIKLGEHLKHPF
ILKRIVGQSGMSYGALGKNAITALSKGLAKAGTWMNTGEGGLSEYHLKGNGDIIFQIGPG
LFGVRDKEGNFSEGLFKEVAQLSNVRAFELKLAQGAKTRGGHMEAEKVNEEIAKIRNVEP
YKTINSPNRYEFIHNAEDLIRFVDQLQQLGQKPVGFKIVVSKVSEIETLVRTMVELDKYP
SFITIDGGEGGTGATFQELQDGVGLPLFTALPIVSGMLEKYGIRDKVKLAASGKLVTPDK
IAIALGLGADFVNIARGMMISVGCIMSQQCHMNTCPVGVATTDAKKEKALIVGEKQYRVT
NYVTSLHEGLFNIAAAVGVSSPTEITADHIVYRKVDGELQTIHDYKLKLIS
LOCUS 62 (H3)
>G2004_STAAU8325, UNDEFINED PRODUCT 1871545:1872954 REVERSE MW:51401
MGIGRVTQVMGPVIDVRFEHNEVPKINNALVIDVPKEEGTIQLTLEVALQLGDDVVRTIA
MDSTDGVQRGMDVKDTGKEISVPVGDETLGRVFNVLGETIDLKEEISDSVRRDPIHRQAP
AFDELSTEVQILETGIKVVDLLAPYIKGGKIGLFGGAGVGKTVLIQELINNIAQEHGGIS
VFAGVGERTREGNDLYFEMSDSGVIKKTAMVFGQMNEPPGARMRVALSGLTMAEYFRDEQ
GQDVLLFIDNIFRFTQAGSEVSALLGRMPSAVGYQPTLATEMGQLQERITSTTKG
LOCUS 63 (GD10)
>G2900_FRG STAAU8325, UNDEFINED PRODUCT 2781950:2783308 FORWARD MW:51966
DPIFKQEVENLEKEIRNV
>G2901_STAAU8325, UNDEFINED PRODUCT 2783589:2784719 FORWARD MW:41914

MMEFTIKRDYFITQLNDTLKAISPRTTLPILTGIKIDAKEHEVILTGSDSEISIEITIPK
TVDGEDIVNISETGSVVLPGRFFVDIIKKLPGKDVKLSTNEQFQTLITSGHSEFNLSGLD
PDQYPLLPQVSRDDAIQLSVKVLKNVIAQTNFAVSTSETRPVLTGVNWLIQENELICTAT
DSHRLAVRKLQLEDVSENKNVIIPGKALAELNKIMSDNEEDIDIFFASNQVLFKVGNVNF
ISRLLEGHYPDTTRLFPENYEIKLSIDNGEFY
LOCUS 64 (F5)
>G1261 FRG_STAAU8325, UNDEFINED PRODUCT 1216923:1217903 FORWARD MW:36061
HTGKVLLVTEDNLEGSIMSEVSAIIAEHCLFDLDAPIMRLAAPDVPSM
PFSPVLENEIMMNPEKILNKMRELAEF
>G1262_STAAU8325, UNDEFINED PRODUCT 1217919:1219190 FORWARD MW:46726
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DTSSNQSSEDNSENSTIPVNGVRKAIAQNMVNSVTEIPHAWMMIEVDATNLVNTRNHYKN
SFKNKEGYNLTFFAFFVKAVADALKAYPLLNSSWQGNEIVLHKDINISIAVADENKLYVP
VIKHADEKSIKGIAREINTLATKARNKQLTAEDMQGGTFTVNNTGTFGSVSSMGIINHPQ
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TNIY
>G1263_STAAU8325, UNDEFINED PRODUCT 1219532:1219978 FORWARD MW:16676
VIELMDMNFDLYMNGVVEQARNEIESAGYEQLTTAEDVDKVLKQDGTTLVMINSVCGCAG
GIARPAASHALHYDVLPDRLVTVFAGQDKEATQRAREYFEGYAPSSPSFALVKDGKITEM
IERHQIEGHDVMNVINQLQTLFNKYCEER
>G1264_STAAU8325, UNDEFINED PRODUCT 1219995:1220972 FORWARD MW:36973
MLKLNPYKIGFRTIKTAVGMTLGVIISKLLGLDNYASSAILVVLCIKHTKVHSLQAIISR
LVSCFLVLFLGSAIFSLLGQSPIVLGIIVLLFIPLTVVLKVQEGVITSCVILLHVFNAKS
IDAHLIVNETLLLLIGLSIAFTMNLMMPSLDKQLDEYKCKIEQQIADIFSKYSYICEKYE
DTIAIEFEVLLLNIKKAKSIAFRDVKNHFVRNENSYYHYFDMREEQVELLMRMKPLIESI
CHKD
LOCUS 65 (F110)
>G2848_STAAU8325, UNDEFINED PRODUCT 2734525:2735082 REVERSE MW:21969
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NIIMMNQNKSNYSIDALYQFLFEFIFDIEERYIRMYVQLSNTPEEFSGNIYGQIQDLNQS
LSKEIAKFYDESKIKMTKEDFQNLILLFLESWYLKASFSQKFGAVEESKSQFKDEVYSLL
NIFLKK
>G2849_STAAU8325, UNDEFINED PRODUCT 2735246:2736481 FORWARD MW:47752
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TIEDTLSNVLALKYEKKEIIIINDGSSDNTAELIYKIKENNDFIFVDLQENRGKANALNQ
GIKQASYDYVMCLDADTIVDQDAPYYMIENFKHDPKLGAVTGNPRIRNKSSILGKIQTIE
YASLIGCIKRSQTLAGAVNTISGVFTLFKKSAVVDVGYWDTDMITEDIAVSWKLHLRGYR

IKYEPLAMCWMLVPETLGGLWKQRVRWAQGGHEVLLRDFFSTMKTKRFPLYILMFEQIIS
ILWVYIVLLYLGYLFITANFLDYTFMTYSFSIFLLSSFTMTFINVIQFTVALFIDSRYEK
KNMAGLIFVSWYPTVYWIINAAVVLVAFPKALKRKKGGYATWSSPDRGNTQR
>G2850_STAAU8325, UNDEFINED PRODUCT 2736448:2736750 FORWARD MW:11783
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LNIENTEILDIFETMGIFAIIIFVFFTISILIQKWQRGRES
>G2851_STAAU8325, UNDEFINED PRODUCT 2736729:2737619 FORWARD MW:34958
MAERKRIVKYRKFIILVLSILIILPVSTLDGHHIANADDDSPKKLKYKENSALALNYHRV
RKANFLNNFIYFFSSSKEIKNYSVSQSQFESQIKWLKSHDAKFLTLKEFLYYKKKGKFPK
RSVWINFDDMDETIYENAYPILKKYKIPATGFIITGHVGEENFHNLDMISKKELKEMYKT
GLWEFETHTHDLHNLSKNNKSKLMKASEATIIKDLNKSEKYLTKNFKKSQKTIAYPYGLM
NDDKLPVIKKAGLKYGFSLEEKAVTPNSNDYYIPRILISDDAFEHLIKRWDGFHEKD
>G2852_STAAU8325, UNDEFINED PRODUCT 2737609:2738658 FORWARD MW:41344
MKKIRLELVYLRAIICAIIIITHLLTQITLKHENMEGGSLVLQFYIRNIVIFGTPCFIIL
SQLLTTLNYQKVTYRYLTTRVKYILIPYILMGLFYSYSESLLTDSSFNKQFIENVLLGQW
YGYFIVVIMQFFILSYIIFKINYNLFNSKILLLLSFILQQSFLYYFTNNTAFHDTVLHYY
PLSENTIIFGWIFYFFLGAYMGYNYERVLNFLERYLVIMIVLAVATYFVFIALANGDYWN
VTSFSYSLTPYNSIMFIVILGICTHFKTMLFNTIQMISAFSFFIYLLHPIILDSLFAYTN
IFEDNTMVFLAISLLFILGLCIGVGMILREFYIFRFIIGKQPYKLNINAY
>G2853_FRG STAAU8325, UNDEFINED PRODUCT 2739111:2741162 REVERSE MW:77120
DPIVLVHGFNGFTDDINPSVLAHYWGGNKMNIRQDLEENGYKAYEASISAFGSNYD
RAVELYYYIKGGRVDYGAAHAAKYGHERYGKTYEGIYKDWKPGQKVHLVGHSMGGQTIRQ
LEELLRNGNREEIEYQKKHGGEISPLFKGNHDNMISSITTLGTPHNGTHASDLAGNEALV
RQIVFDIGKMFGNKNSRVDFGLAQWGLKQKPNESYIDYVKRVKQSNLWKSKDNGFYDLTR
EGATDLNRKTSLNPNIVYKTYTGEATHKALNSDRQKADLNMFFPFVITGNLIGKATEKEW
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LOCUS 66 (E1)
>G0406_STAAU8325, UNDEFINED PRODUCT 370166:372094 REVERSE MW:70979
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EKIKKEHKNFIFGEGVSRGKILAALLFGMFIAILNQTLLNVALPKINTEFNISASTGQWL
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FIIGIIAILIGFVWFKLYQYTTNPKADIPGIIFSTIGFGALLYGFSEAGNKGWGSVEIET
MFAIGIIFIILFVIRELRMKSPMLNLEVLKFPTFTLTTIINMVVMLSLYGGMILLPIYLQ
NLRGFSALDSGLLLLPGSLIMGLLGPFAGKLLDTIGLKPLAIFGIAVMTYATWELTKLNM
DTPYMTIMGIYVLRSFGMAFIMMPMVTAAINALPGRLASHGNAFLNTMRQLAGSIGTAIL
VTVMTTQTTQHLSAFGEELDKTNP
>G0407_STAAU8325, UNDEFINED PRODUCT 372110:372754 REVERSE MW:23024
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DDLYVTANIDEKDIKDVEVGKDVDVTIDGQKASIKGKVDSIGKATAASFSLMPSSNSDGN
YTKVSQVIPVKITLESEPSKQVVPGMNAEVKIHKN
LOCUS 67 (F119)
>G1831 FRG_STAAU8325, UNDEFINED PRODUCT 1723090:1723806 REVERSE MW:27770
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KELKNVTGYRYSKGGKHYLIFDKNRKFTRVQIFGKDIERFKARKNPGLDIFVVKEAENRN
GTVFSYGGVTKKNQDAYYDYINAPRFQIKRDEGDGIATYGRVHYIYKEEISLKELDFKLR
QYLIQNF
>G1832_STAAU8325, UNDEFINED PRODUCT 1724158:1725096 REVERSE MW:34671
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VHRNVDVFVVLEENNYNLEKYSVGGITKSNSKKVDHKAGVRITKEDNKGTISHDVSEFKI
TKEQISLKELDFKLRKQLIEKNNLYGNVGSGKIVIKMKNGGKYTFELHKKLQENRMADVI
DGTNIDNIEVNIK
>G1834_STAAU8325, UNDEFINED PRODUCT 1725193:1725327 REVERSE MW:5264
LFVKVAFLCLKSDETSNVPSVESHQNHFYLTNIMDFLIYLTMIQI
>G1835_STAAU8325, UNDEFINED PRODUCT 1725449:1726531 REVERSE MW:40775
LEHTIMKMRTIAKTSLALGLLTTGAITVTTQSVKAEKIQSTKVDKVPTLKAERLAMINIT
AGANSATTQAANTRQERTPKLEKAPNTNEEKTSASKIEKISQPKQEEQKTLNISATPAPK
QEQSQTTTESTTPKTKVTTPPSTNTPQPMQSTKSDTPQSPTIKQAQTDMTPKYEDLRAYY
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DNKYQLKKYSVGGITKTNSKKVNHKVELSITKKDNQGMISRDVSEYMITKEEISLKELDF
KLRKQLIEKHNLYGNMGSGTIVIKMKNGGKYTFELHKKLQEHRMADVIDGTNIDNIEVNI
K
>G1837_STAAU8325, UNDEFINED PRODUCT 1726810:1727562 REVERSE MW:28926
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IDRIEIKVIKA
LOCUS 68 (G27)
>G0516_STAAU8325, UNDEFINED PRODUCT 482272:486597 REVERSE MW:163057
VVIVLAMTEQQKFKVLADQIKISNQLDAEILNSGELTRIDVSNKNRTWEFHITLPQFLAH
EDYLLFINAIEQEFKDIANVTCRFTVTNGTNQDEHAIKYFGHCIDQTALSPKVKGQLKQK
KLIMSGKVLKVMVSNDIERNHFDKACNGSLIKAFRNCGFDIDKIIFETNDNDQEQNLASL
EAHIQEEDEQSARLATEKLEKMKAEKAKQQDNNESAVDKCQIGKPIQIENIKPIESIIEE
EFKVAIEGVIFDINLKELKSGRHIVEIKVTDYTDSLVLKMFTRKNKDDLEHFKALSVGKW
VRAQGRIEEDTFIRDLVMMMSDIEEIKKATKKDKAEEKRVEFHLHTAMSQMDGIPNIGAY
VKQAADWGHPAIAVTDHNVVQAFPDAHAAAEKHGIKMIYGMEGMLVDDGVPIAYKPQDVV
LKDATYVVFDVETTGLSNQYDKIIELAAVKVHNGEIIDKFERFSNPHERLSETIINLTHI

TDDMLVDAPEIEEVLTEFKEWVGDAIFVAHNASFDMGFIDTGYERLGFGPSTNGVIDTLE
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NKKLSNEDAYKRARPSHVTLIVQNQQGLKNLFKIVSASLVKYFYRTPRIPRSLLDEYREG
LLVGTACDEGELFTAVMQKDQSQVEKIAKYYDFIEIQPPALYQDLIDRELIRDTETLHEI
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LOCUS 69 (H110)
>G2217 FRG_STAAU8325, UNDEFINED PRODUCT 2108154:2110211 FORWARD MW:74420
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AKPENKKVVAGLMGSAALTSFLTGITEPLEFSFLFVAPLLFFIHAVLDGLSFLTLYLLDL
HLGYTFSGGFIDYFLLGILPNKTQWWLVIPVGLVYAVIYYFVFRFLIVKLKYKTPGREDK
QSQAATASATELPYAVLEAMGGKANIKHLDACITRLRVEVNDKSKVDVPGLKDLGASGVL
EVGNNMQAIFGPKSDQIKHEMQQIMNGQVVENPTTMEDDKDETVVVAEDKSATSELSHIV
HAPLTGEVTPLSEVPDQVFSEKMMGDGIAIKPSQGEVRAPFNGKVQMIFPTKHAIGLVSD
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LOCUS 70
>G1778_STAAU8325, UNDEFINED PRODUCT 1669401:1669715 REVERSE MW:11597
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AVDPDDIEMLQDLVLAATNEAMNKADELTQERLGKHTQG
>G1780_STAAU8325, UNDEFINED PRODUCT 1669808:1671502 REVERSE MW:63481
LNYQALYRMYRPQSFEDVVGQEHVTKTLRNAISKEKQSHAYIFSGPRGTGKTSIAKVFAK
AINCLNSTDGEPCNECHICKGITQGTNSDVIEIDAASNNGVDEIRNIRDKVKYAPSESKY
KVYIIDEVHMLTTGAFNALLKTLEEPPAHAIFILATTEPHKIPPTIISRAQRFDFKAISL
DQIVERLKFVADAQQIECEDEALAFIAKASEGGMRDALSIMDQAIAFGDGTLTLQDALNV
TGSVHDEALDHLFDDIVQGDVQASFKKYHQFITEGKEVNRLINDMIYFVRDTIMNKTSEK
DTEYRALMNLELDMLYQMIDLINDTLVSIRFSVNQNVHFEVLLVKLAEQIKGQPQVIANV
AEPAQIASSPNTDVLLQRMEQLEQELKTLKAQGVSVAPVQKSSKKPARGIQKSKNAFSMQ
QIAKVLDKANKADIKLLKDHWQEVIDHAKNNDKKSLVSLLQNSEPVAASEDHVLVKFEEE
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AQQTDIAQKAKDLFGEETVHVIDEE
>G1781_STAAU8325, UNDEFINED PRODUCT 1671574:1672095 REVERSE MW:19908
MQIYLSTLTELDYDKSLNSIEESFDDNPETSWQARAKVKHLRKSPCYNFELEVIAKNENN
DVVGHVLLIEVEINSDDKTYYGLAIASLSVHPELRGQKLGRGLVQAVEERAKAQEYSTVV
VDHCFDYFEKLGYQNAAEHDIKLESGDAPLLVKYLWDNLTDAPHGIVKFPEHFY
>G1782_STAAU8325, UNDEFINED PRODUCT 1672236:1672334 REVERSE MW:3948
LKTIQRIIRGTCLWEVAFLYVKFDSSELDVQFE

>G1783_STAAU8325, UNDEFINED PRODUCT 1672737:1673480 REVERSE MW:28585
IGNDVASDSIYDYLEKVLNL
NISYSSKSITFEPFDEQAYQLFGDVSVAYSATVRSIVYLENTMPFQYNISKHLANEFKFN
DFSRRRIK
LOCUS 71
>G1083_STAAU8325, UNDEFINED PRODUCT 1057165:1058778 REVERSE MW:57664
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YQKVSEIEAEGDIETGVNIVLKALTAPVRQIAENAGLEGSVIVERLKNAEPGVGFNAATN
EWVNMLE
LOCUS 72
>G2296_STAAU8325, UNDEFINED PRODUCT 2195143:2196150 REVERSE MW:37749
MNREMLYLNRSDIEQAGGNHSQVYVDALTEALTAHAHNDFVQPLKPYLRQDPENGHIADR
IIAMPSHIGGEHAISGIKWIGSKHDNPSKRNMERASGVIILNDPETNYPIAVMEASLISS
MRTAAVSVIAAKHLAKKGFKDLTIIGCGLIGDKQLQSMLEQFDHIERVFVYDQFSEACAR
FVDRWQQQRPEINFIATENAKEAVSNGEVVITCTVTDQPYIEYDWLQKGAFI
>G2297_STAAU8325, UNDEFINED PRODUCT 2196150:2197127 REVERSE MW:35879
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VAPVSTTGSIMGMSRKIKEVHPNAQIVAVDAKGSVIFGDKPINRELPGIGASRVPEILNR
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LOCUS 73
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KPALARGELQCIGATTLDEYRKNIEKDAALERRFQPVQVDEPSVVDTVAILKGLRDRYEA
HHRINISDEAIEAAVKLSNRYVSDRFLPDKAIDLIDEASSKVRLKSHTTPNNLKEIEQEI
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AGWTGIPLTKINETESEKLLSLEDTLHERVIGQKDAVNSISKAVRRARAGLKDPKRPIGS
FIFLGPTGVGKTELARALAESMFGDDDAMIRVDMSEFMEKHAVSRLVGAPPGYVGHDDGG
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GAQELQD
LOCUS 74
>G1438_STAAU8325, UNDEFINED PRODUCT 1399373:1401364 REVERSE MW:74364
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AKGEATDECTDIYSIGIVLYEMLVGEPPFNGETAVSIAIKHIQDSVPNVTTDVRKDIPQS
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TPNTGERVERGDSVDVVISKGPEKVKMPNVIGLPKEEALQKLKSLGLKDVTIEKVYNNQA
PKGYIANQSVTANTEIAIHDSNIKLYESLGIKQVYVEDFEHKSFSKAKKALEEKGFKVES
KEEYSDDIDEGDVISQSPKGKSVDEGSTISFVVSKGKKSDSSDVKTTTESVDVPYTGKND
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>G1439_STAAU8325, UNDEFINED PRODUCT 1401364:1402104 REVERSE MW:28046
DQLMQLALDNHSKDNVTFILA
AIEGDKV
LOCUS 75
>G0364_STAAU8325, UNDEFINED PRODUCT 331693:334395 REVERSE MW:98970
MAANFKEQSKKHFDLNGQSYTYYDLKAVEEQGITKVSNLPYSIRVLLESLLRQEDDFVIT
DDHIKALSQFGKDGNEGEVPFKPSRVILQDFTGVPAVVDLASLRKAMDDVGGDITKINPE
VPVDLVIDHSVQVDSYANPEALERNMKLEFERNYERYQFLNWATKAFDNYNAVPPATGIV
HQVNLEYLASVVHVRDVDGEKTAFPDTLVGTDSHTTMINGIGVLGWGVGGIEAEAGMLGQ
PSYFPIPEVIGVRLVNSLPQGATATDLALRVTQELRKKGVVGKFVEFFGPGVQHLPLADR
ATIANMAPEYGATCGFFPVDDESLKYMKLTGRSDEHIALVKEYLKQNHMFFDVEKEDPNY
TDVIELDLSTVEASLSGPKRPQDLIFLSDMKSSFENSVTAPAGNQGHGLDKSEFDKKAEI
NFKDGSKATMKTGDIAIAAITSCTNTSNPYVMLGAGLVAKKAVEKGLKVPEYVKTSLAPG
SKVVTGYLRDAGLQPYLDDLGFNLVGYGCTTCIGNSG
LOCUS 76
>G2434_STAAU8325, UNDEFINED PRODUCT 2324870:2325844 REVERSE MW:37506
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KDKPISDYPVYEMRWDIGYVLQQIALFPHMTIKENIAQVPQMKKWKEKDIDKRVDELLEM
VGLEPEKYKNRKPDELSGGQRQRVGVIRALAADPPVILMDEPFSALDPISREKLQDDLIE
LQTKIKKTIIFVTHDIQEAMKLGDKICLLNEGHIEQIDTPEGFKNNPQSEFVKQFMGSHL
EDDAPCVEENA
>G2435_STAAU8325, UNDEFINED PRODUCT 2326069:2327847 REVERSE MW:68170
HGLMKGYTTSELSHLIDELRFKGFLNENDEI
LMCDTSIKKLLSNEVEVFTTPFKQKATEKVFINTVEGVDRVLFSQLVEVRKKLSDKLTIA
PVSIFSDYTLEEFAKRKPASKQDMINIDGVGSYKLKHYCPAFLETIQNYKAKV
LOCUS 77
>G2617_STAAU8325, UNDEFINED PRODUCT 2501985:2502917 REVERSE MW:34781
DRAIRSVAFFLTALPSYWIASILIIYVSVKLNILPTSGLTGP

LOCUS 78

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RLEGVINFENLKVKDVDTTPRINVTAFASNATYEEVYETVMNKPYTRYPVYEGDIDNIIG
VFHSKYLLAWSNKKENQITNYSAKPLFVNEHNKAEWVLRKMTISRKHLAIVLDEFGGTEA
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LOCUS 79

>G1981_STAAU8325, UNDEFINED PRODUCT 1853885:1855240 REVERSE MW:50053
MINVTLKQIQSWIPCEIED

>G1982_STAAU8325, UNDEFINED PRODUCT 1855258:1856436 REVERSE MW:44485
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LOCUS 80

MEROZOITE SURFACE ANTIGEN

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SURFACE PROTEIN

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G0745
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LOCUS 86
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LOCUS 103 (GF11)
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>G2236_STAAU8325, UNDEFINED PRODUCT 2134482:2135219 REVERSE MW:28095
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EPEYYL
LOCUS 104 (GF12)
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FORWARD MW:37832
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LOCUS 111
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LOCUS 112
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LOCUS 113
G1111
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LOCUS 114
G1542
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G1543
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G1546
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G2715

>G2715_STAAU8325, UNDEFINED PRODUCT 2602253:2603800 REVERSE MW:57130

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TABLE 9 DNA SEQUENCES STAPHYLOCCOCUS EPIDERMIDIS

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LOCUS 4:
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LOCUS 5:

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LOCUS 6:
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LOCUS 7:
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LOCUS 8:
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LOCUS 9:
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LOCUS 10:
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LOCUS 11:
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TCAGTTACTTTAAAAAGTTGATC
LOCUS 12:
GATCCTGACACAGCTATTTCTCTCTTAGATAATC
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AAATCGAGACTTTCAATTGATTTGCTATTTCGCAGTATGTGTCCAGTCATGTTTTCCTTT
ATAGCGTTTAACATGTGCATATACTTGATC

TABLE 10 PROTEIN SEQUENCE STAPHYLOCOCCUS EPIDERMIDIS

LOCUS 1:
ORF1:
DQTALKQAEKAKSEVTQSTTNVSGTQTYQDPTQVQPKQDTQSTTYDASLDEMSTYNEISS
NQKQQSLSTDDANQNQTNSVTKNQQEETNDLTQEDKTSTDTNQLQETQSVAKENEKDLGA
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NFDYDDEDDDSSTDHLEPISLNNVNATSKQTTSYKYKEPAQRVTTNTVKKETASNQATID
TKQFTPFSATAQPRTVYSVSSQKTSSLPKYTPKVNSSINNYIRKKNMKAPRIEEDYTSYF
PKYGYRNGVGRPEGIVVHDTANDNSTIDGEIAFMKRNYTNAFVHAFVDGNRIIETAPTDY
LSWGAGPYGNQRFINVEIVHTHDYDSFARSMNNYADYAATQLQYYNLKPDSAENDGRGTV
WTHAAISNFLGGTDHADPHQYLRSHNYSYAELYDLIYEKYLIKTKQVAPWGTTSTKPSQP
SKPSGGTNNKLTVSANRGVAQIKPTNNGLYTTVYDSKGHKTDQVQKTLSVTKTATLGNNK
FYLVEDYNSGKKYGWVKQGDVVYNTAKAPVKVNQTYNVKAGSTLYTVPWGTPKQVASKVS
GTGNQTFKATKQQQIDKATYLYGTVNGKSGWISKYYLTTASKPSNPTKPSTNNQLTVTNN
SGVAQINAKNSGLYTTVYDTKGKTTNQIQRTLSVTKAATLGDKKFYLVGDYNTGTNYGWV
KQDEVIYNTAKSPVKINQTYNVKPGVKLHTVPWGTYNQVAGTVSGKGDR

LOCUS 2:
ORF1:
RIGGKYMDNIKIIVASDSIGETAELVARAGVSQFNPKQCKHEFLRYPYIESFENVDEVIQ
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RLDDAYFKKIDAIEFAVKYDDGKDR
ORF2:
GEAFMVKNMDTIVQLAKHRGFVFPGSDIYGGLSNTWDYGPLGVELKNNIKKAWWQKFITQ
SPYNVGIDAAILMNPKTWEASGHLGNFNDR
ORF3:
RPIELSQRQEQIIEIVKSEGPITGEHIAEKINLTRATLRPDLAILTMSGFIEARPRVGYF
YSGKSKNKIINEKLRKYVVKDYMSHPVVIKENMTVYDAICTIFLEDVSTLFITNENNDFV
GVCSRKDLLRASMIGEDIHTMPISVNMTRMPHVSYLKEQELVIYAANQMIDKEIDSLPIV
RPKENDKFEVIGRISKTTITKLFVSLFKE

LOCUS 3:
ORF1:

SVMKNFILSVQHLLAMYAGAILVPIIVGTSLKFSAEEIAYLVTVDIFMCGVATFLQANKV
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NLLIIAISVGLGAGISAVPQAFKGLGEQFAWLTQNGIVLGAISAIILNFFFNGIKYKQTE
ENVK
ORF2:
VESLGRKVKEDGVVIDEKILKVDGFLNHQIDAKLMNDVGKTFYESFKDAGITKILTIEAS
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LIIDDFLANGDASLGLNDIVKQANATTVGVGIVVEKSFQNGRQRLEDAGLYVSSLCKVAS
LKGNKVTLLGEA
ORF3:
NWRLFLMWENKFAKESLTFDDVLLIPAASDVLPSDVDLSVKLSDKI
LOCUS 4:
ORF1:
YWTYHFKEKGKMVIMDDLKQNQSSNEKPKGNKIINILIFIGMILLIQIPIGVSLIALPFS
VKFSKLTSIALSMLITGTALLIIWLVRNYYLSHTYERQYQSMRGKDIFINIGFLVLSMVF
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FRGIFKETLFMKYRFWLPFIISSIIFSSQHLSTNIFSYAIYFLMGCVLYLAYNRRRNIKD
SMMVHMLNNSVSTLPVFVGYLWLYFR
ORF2:
DLHIIKGDTPEVKSHTTLGHEGIGIIEEIGDNVNNFKVGDKVIISCISSCGKCYYCKKGI
YAHCENGGGWILGHLVNGTQAEYVKVPFADNSLYHAPSNLKEDALVMLSDILPTGYEIGV
LKGKVKPGCTVAIVGAGPVGLAALLTAQFYSPSKIIMIDLDDNRLETAKELGATHLINSK
ETETAIKKVKSLNPRGVDVAIEAVGIPQTFDLCQNLIGVDGTIANVGVHGLPVQLDIDKL
WIKNINVTTGLVSGNTTEELLEALKSKIIQPEQLVTHYSKLSEIESAYDLFRNATDHKAI
KLIIENDITI
LOCUS 5:
ORF1:
QIVQRKGCHLMKIRVIVPCYNEGEVVLKTYDKLTEIMKKDSLIKNYEYDLLFINDGSTDT
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ALTTLDEYNRFSKGLFEWIGYETKVFQYENVTREDGESKWTFRKLLNYGIDGLISFNNKP
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DTYASNYSQDEGFKERVH
ORF2:
DQLLVNILQPYEQHIKQENRTLEVNFCTDIDAFYQYRPPIERILTNLLDNALKFSNSGSR
IDIIISECKENDVISISIKDEGIGIVPELQSRIFERTFRVEDSRNTKTGGSGLGLYIANE
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LOCUS 6:
ORF1:
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ORF2:
GGVTLKKLAFAITAASGAAAVLSHHDAEASTQHKVQSGESLWTIAQQYNTSVESIKQNNN

LSNNMVFPGQVINVGGSASQNTSSNTSSSSASSHTVVAGESLNIIANKYGVSVDALMQAN
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ISEMNYANGPYNMNYRTIPASEVSSYAFIH
LOCUS 7:
ORF1:
DHIIRAYHKFLQSGYQTELHLFGRDEDNQIPLMNTLISELKLSDKVKIFKYTNQPLQEFK
NSKASLLTSQYEGFGLTLMESIEMGCPVLSYNVRYGPSEIIQNGINGYLIEKNDIDSLSK
HMINIIEHPLQKVKNKDTLKYNAAVNNYKQLMQSLDLLK
ORF2:
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VSEMNWSAAPGNMTYRTIPAYQVRNYKFIH
LOCUS 8:
ORF1:
DQFREAMTKFPVWMGATTLFFGAINGAKEMLDVITEIDGKMITLAKVTGDDNALQQTFID
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SAQWETTGNQAMRQVDSLNEVSNKYATTVEKLAQGQAKAGSTAKSMGLTFDETNGIIGAL
TAKTKQSGDEIGNFMKATLPKLYSGKGKSTIEGLGISMKDENGQLKSAISLLEEVSQKTK
NLEKDQKAAVINGLGGTYHYQRMQVLLDDLSKTDGLYKQIKESSESSAGSALQENAKYME
SIEAKVNQAKTAFEQFALAVGETFAKSGMLDGIRMVTQLLTGLTHGITELGTTAPIFGMV
GGAASLMSKNVRSGFEGARSSVANYITEVNKLAKVNNAAGQVVGLQKVQTGTASQLQFNK
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EVMKQKIELIKQEMELERQKNAIKQKEEQDAYIKEQDSLAKKNRGQKWYQLGQTPELKLQ
EQARPTTVSDNSNINKINATIQKVKSQAQAEKALEQVDKQLAQSQTKNRQNEVQHLQKVR
QALQDYITKTGQANQATRAAVLTAQQQFTNQIATMKKLGTTGQQVMTTISNSVAKTAKSG
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IMQAAKAANMSKSQMKDLKKSLQQNIQAETGFRASVSKAGKVTIDQSKKIKQNR
LOCUS 9:
ORF1:
VLWGVFDMDLLIGTLFLILVLVIFTLFTYKAPSGMRAMGALANAAIASFLVEAFNKYVGG
QVFGIKFLEELGDAAGGLGGVAAAGLTALAIGVSPVYALVIGAACGGMDLLPGFFAGYIV
GYMMKYTEKYVPDGIDLIGSIILLAPIARLIATGLTPVVNNTLIKIGDIIQSSTDANPLI
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FGFNSLTKVIIYGVVMAIIGTIAGIVGSIVFKKYPIITKKQMLERDTTT
LOCUS 10:
ORF1:
MEIKQIKYFVEVVRQGGMTQASEHLYIAQSTISKAIKNIENEYDITLFDRSQKQIKLTDI
GQTFYDNSLEFLALFEKLSLEMNDIVNVQKGHIKIGLSPMMNVQMFTNALNQFHRLYPNV
TYEVIEGGGKIVENLTSNDDVDIGITTLPVDL
ORF2:
LSESANSFYLHVDDFLIRIVKECLLTHVNSKLMLWRFVMGSFFNRMTRKENPTIYQNKDG
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LPKSLSNPFGSNGGVIDIIAAVVIILTALLLSRGMNEAARMENVLVILKVLAIILFVIVG
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LOCUS 11:
ORF1:
DPETLFIVMSQILFHPLVGGFLLAAILAAIMSTISSQLLVTSSSLTEDFYKLIRGSDKAS
SHQKEFVLIGRLSVLLVAIVAITIAWHPNDTILNLVGNAWAGFGAAFSPLVLYSLYWKDL
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DYVIENLNKVKHVVKE
ORF2:
DQLFKVTESELIEIQDIGDKLAQSVVTYLENSDIRSLIEKLSNKNVNMSYKGIKTTEIEG
HPDFSGKTIVLTGKLEQMTRNEASEWLKMQGAKVTNSVTKSTDIVIAGADAGSKLAKAEK
YGTEIWTEAAFIEKQNGI
ORF3:
MKRTIFLLMSILLLLTACGDGHKQTSSDKEQSEHKDNHNKNQVKQIATDKKVQGDNYRTI
LPFKESQARGLLQDNMANGYNGEDFESGLLELSKEIFPTNKYLYQDGQYLDKKTINAYLD
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LKDIPIHFAIYKQSSQDSITPGEFIVGTTVEEGKTKINSWDNINEKAALIPSSTAADYDE
TLNNNFKQFNDNLQSYFSNFTQAVGKVKFVNKKAKQLTVDLPIDYYGQAETIGITQYVTE
QAEKYFDKLDEYEIRIKDGNTPRALISKTKDDKEPQVHIYHN
LOCUS 12:
ORF1:
LDTSKGQSSMEEVLKLKIPASTANLGVGFDSIGMALDKYLHMSIRKIERANWEFLYYSSE
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FGNIQLSKYELLQLATEIEGHPDNVAPTIYGGLIAGFYNPITKITDVARIEVPHVDIILT
IPPYELRTEDSRRVLPDTFSHKGAVQNSAISNTMICALIQHKYKLAGKMMEQDGFHEPYR
QHLIPEFNQVRKLSRQHDAYATVISGAGPTILTLCPKEKSGKLVRTLREKINNCASELVT
INEIGVKDEVVYLKS
ORF2:
LLKGVLYYMTQYKMVVLDMDDTLMNSDNKLSIETKSYLLDIQKRGYYVVLASGRPTEGML
PTARELELNKYNSFIISYNGGKTINMANENVEVDQPVSKEDFDNIVDYCRDKNFLVLTYD
NGYIIHDSSHEYMNIESQLTGLPMNRVADLKEYINHSVPKVMGVDYVGHITEARIELDGY
FNNDIDVTTSKPFFLEFMAKNVSKGNAIKALCKRLQISLEEVIVFGDSLNDKSMFEVAGY
SVAMGNASDELKKIADEVTLDNNSNGIPYALKELLV

CLAIMS

1. An antigenic polypeptide, or part thereof, encoded by an isolated DNA molecule selected from the group consisting of:

(i) DNA molecules represented by the DNA sequences in Table 7 or 9;

(ii) DNA molecules which hybridize to the sequences identified in (i) which encode a polypeptide expressed by a pathogenic organism; and

(iii) DNA molecules which are degenerate as a result of the genetic code to the DNA sequences defined in (i) and (ii),

for use as a vaccine.

2. An antigenic polypeptide according to Claim 1 wherein said DNA molecule is genomic DNA.

3. An antigenic polypeptide according to Claim 1 or 2 wherein said DNA molecule hybridizes to the the sequences in Tables 7 or 9 under stringent hybridization conditions.

4. An antigenic polypeptide according to any of Claims 1-3 wherein said polypeptide (s) are represented by the amino acid sequences in Tables 8 or 10.

5. An antigenic polypeptide according to any of Claims 1-4 wherein said polypeptide is derived from a bacterial genus/species selected from the group consisting of: *Staphylococcus spp.; Staphylococcus aureus; Staphylococcus epidermidis; Enterococcus faecalis; Mycobacterium tuberculsis; Streptococcus group B; Streptoccocus pneumoniae; Helicobacter pylori; Neisseria gonorrhea; Streptococcus group A; Borrelia burgdorferi; Coccidiodes immitis; Histoplasma sapsulatum; Neisseria meningitidis type B; Shigella flexneri; Escherichia coli; Haemophilus influenzae.*

6. An antigenic polypeptide according to Claim 5 wherein said polypeptide is derived from the genus *Staphylococcus spp.*

7. An antigenic polypeptide according to Claim 6 wherein said polypeptide is derived from the species *Staphylococcus aureus.*

8. An antigenic polypeptide according to Claim 6 wherein said polypeptide is derived from the species *Staphylococcus epidermidis.*

9. An antigenic polypeptide according to any of Claims 1-8 wherein said polypeptide is an opsonin.

10. A vaccine composition comprising at least one antigenic polypeptide according to any of Claims 1-9.

11. A vaccine composition according to Claim 10 wherein said composition further comprises a carrier and/or an adjuvant.

12. A method to immunize an animal against a disease or condition caused by a pathogenic microbe comprising administering to said animal at least one antigenic polypeptide according to any of Claims 1-9 or a vaccine composition according to Claim 10 or 11.

13. A method according to Claim 12 wherein said animal is human.

14. A method according to Claim 12 or 13 wherein said disease or condition is selected from the group consisting of: bacterimia; septic shock; organ infection; skin infection; bacterial nasal colonisation; bacterial eye infections; septicaemia; tuberculosis; bacteria-associated food poisoning; blood infections; peritonitis; endocarditis; sepsis; meningitis; pneumonia; stomach ulcers; gonorrhoea; strep throat; streptococcal-associated toxic shock; necrotizing fasciitis; impetigo;

histoplasmosis; Lyme disease; gastro-enteritis; dysentery; shigellosis; *Staphylococcus aureus*-associated septicaemia, food-poisoning or skin disorders; *Staphylococcus epidermidis*-associated septicaemia, peritonitis or endocarditis.

15. A method according to Claim 14 wherein said disease or condition is the result of a *Staphylococcus spp* infection.

16. A method according to Claim 15 wherein said disease or condition is *Staphylococcus aureus*-associated septicaemia, food-poisoning or skin disorders.

17. A method according to Claim 15 wherein said disease or condition is *Staphylococcus epidermidis*-associated septicaemia, peritonitis or endocarditis.

18. An antibody, or binding part thereof, obtainable by the method according to any of Claims 12-17.

19. An antibody according to Claim 18 wherein said antibody is a monoclonal antibody.

20. An antibody according to Claim 18 or 19 wherein said antibody is a chimeric antibody.

21. An antibody according to Claim 18 or 19 wherein said antibody is a humanized antibody.

22. An antibody according to any of Claims 18-21 wherein said antibody is an opsonic antibody.

23. An antibody according to any of Claims 18-22 wherein said antibody is a therapeutic antibody or a diagnostic antibody.

24. A method for preparing a hybridoma cell-line producing monoclonal antibodies according to Claim 19 comprising the steps of:

i) immunising an immunocompetent mammal with an immunogen comprising at least one polypeptide having the amino acid sequence as represented in Tables 8 or 10, or polypeptide fragments thereof;

ii) fusing lymphocytes of the immunised immunocompetent mammal with myeloma cells to form hybridoma cells;

iii) screening monoclonal antibodies produced by the hybridoma cells of step (ii) for binding activity to the amino acid sequences of (i);

iv) culturing the hybridoma cells to proliferate and/or to secrete said monoclonal antibody; and optionally

v) recovering the monoclonal antibody from the culture supernatant.

25. A method according to Claim 24 wherein said hybridoma cell-line produces opsonic antibodies.

26. A hybridoma cell-line produced by the method of Claim 24 or 25.

27. A method to identify opsonic antigens expressed by a pathogenic microbe comprising:

i) providing a host cell transformed with a DNA library encoding genes, or partial gene sequences, of a pathogenic microbe;

ii) providing conditions conducive to the expression of said transformed genes or partial sequences;

iii) contacting the antigens expressed by said gene sequences with autologous antisera derived from an animal infected with, or has been infected with, said pathogenic microbe;

iv) purifying the DNA encoding antigenic polypeptides binding to said autologous antisera; and

v) testing the opsonic activity of a polypeptide encoded by said DNA molecule.